

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:42:53 ; Search time 21.0928 Seconds
(without alignments)
1806.392 Million cell updates/sec

Title: US-10-732-923-406
Perfect score: 2118
Sequence: 1 MTVTIKELTNHNYIDHELSEA.....KIVYDLDYHLFYMKLQKXI 396
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118	100.0	396	1	DCBYDM
2	479	22.6	333	1	adenosylmethionine
3	479	22.6	334	1	adenosylmethionine
4	478	22.6	334	2	adenosylmethionine
5	476	22.5	335	2	adenosylmethionine
6	470	22.2	334	1	adenosylmethionine
7	434	20.5	368	2	adenosylmethionine
8	404	19.1	362	2	adenosylmethionine
9	401.5	19.0	353	2	adenosylmethionine
10	398.5	18.8	357	2	adenosylmethionine
11	387	18.3	369	2	adenosylmethionine
12	378	17.8	393	2	adenosylmethionine
13	376.5	17.8	381	2	adenosylmethionine
14	372.5	17.6	400	2	adenosylmethionine
15	359	16.9	361	2	adenosylmethionine
16	348.5	16.5	377	2	adenosylmethionine
17	343	16.2	360	2	adenosylmethionine
18	341.5	16.1	361	2	adenosylmethionine
19	331	15.6	363	2	adenosylmethionine
20	313	14.8	398	2	adenosylmethionine
21	110.5	5.2	900	2	adenosylmethionine
22	108	5.1	1576	1	adenosylmethionine
23	107	5.1	1034	2	adenosylmethionine
24	106.5	5.0	1028	2	adenosylmethionine
25	104	4.9	958	2	adenosylmethionine
26	103	4.9	1126	2	adenosylmethionine
27	102.5	4.8	1004	2	adenosylmethionine
28	101	4.8	518	2	adenosylmethionine
29	100.5	4.7	773	2	adenosylmethionine

hypothetical prote
virb4 protein prec
hypothetical prote
protein containing
hypothetical prote
hypothetical prote
E2 protein - human
acridine resist
urate oxidase (EC
ADPglyceromanno-he
hypothetical prote
conserved hypothet
Lian-Aal retrotran
polyadenylate-bind
exodeoxyribonuclea
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

DCBYDM

adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O1275; protein YOL052c
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 09-Jul-2004
C;Accession: S12772; A30469; S59299; S61729; S66737; S66744
R;Kashiwagi, K.; Taneja, S.K.; Liu, T.Y.; Tabor, C.W.; Tabor, H.
J. Biol. Chem. 265, 22321-22328, 1990
A;Title: Spermidine biosynthesis in Saccharomyces cerevisiae. Biosynthesis and processing
A;Reference number: S12772; MUID:91093074; PMID:2266128
A;Accession: S12772
A;Molecule type: DNA
A;Residues: 1-396 <KAS1>
A;Cross-references: UNIPROT:P21182; EMBL:M38434; NID:gl71054; PIDN:AAA34421.1; PID:gl710
A;Accession: A30469
A;Molecule type: protein
A;Residues: 2-19,'A',89-101,'X',103-104 <KAS2>
R;Mannhaupt, G.; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.
submitted to the EMBL Data Library, August 1995
A;Description: Analysis of a 26kb region on the left arm of yeast chromosome XV.
A;Reference number: S59285
A;Accession: S59299
A;Molecule type: DNA
A;Residues: 1-396 <PEL>
A;Cross-references: EMBL:X91067; NID:g984177; PIDN:CAA62536.1; PID:g984192
R;Mannhaupt, G.; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.
Yeast 12, 67-76, 1996
A;Title: Analysis of a 26 kb region on the left arm of yeast chromosome XV.
A;Reference number: S61715; MUID:96381248; PMID:8789261
A;Accession: S61729
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-396 <MAN>
A;Cross-references: EMBL:X91067; NID:g984177; PIDN:CAA62536.1; PID:g984192
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Ansgorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66737
A;Accession: S66737
A;Molecule type: DNA
A;Residues: 1-396 <ANS>
A;Cross-references: EMBL:Z74794; NID:gl1419858; PIDN:CAA99058.1; PID:gl1419859; GSPDB:GN000
A;Experimental source: strain S288C
R;Feldmann, H.; Mannhaupt, G.; Vetter, I.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66743
A;Accession: S66744
A;Molecule type: DNA
A;Residues: 1-396 <FEW>
A;Cross-references: EMBL:Z74794; NID:gl1419858; PIDN:CAA99058.1; PID:gl1419859; GSPDB:GN000
A;Experimental source: strain S288C

C;Comment: The pyruvyl group derived from 88-Ser is required for catalytic activity and C;Genetics:

A;Gene: SGD:SPE2; MIPS:YOL052C
A;Cross-references: SGD:S0005412; MIPS:YOL052C
A;Map position: 15L

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase; polyamine biosynthesis
F;2-87/Domain: beta chain #status experimental <CHB>
F;2-87/88-396/Product: adenosylmethionine decarboxylase #status experimental <MAT>
F;88-396/Domain: alpha chain #status experimental <CHA>
F;88/Modified site: pyruvic acid (Ser) (in mature form) #status experimental

Query Match 100.0%; Score 2118; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 7e-154; Indels 0; Gaps 0;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTVTIKELTNHNTIDHLSATLSDTAPEGEPEKLEIWFPPHKKSIITTEKTLNIGMDRW 60
Db 1 MTVTIKELTNHNTIDHLSATLSDTAPEGEPEKLEIWFPPHKKSIITTEKTLNIGMDRW 60

Qy 61 IEILKLVKCVLSMKTKELDALLSSSLFVFDHKLTKTCTTTTLFCLEKLFQIVEQ 120
Db 61 IEILKLVKCVLSMKTKELDALLSSSLFVFDHKLTKTCTTTTLFCLEKLFQIVEQ 120

Qy 121 ELSWAFRTTGGKYKPKFVSRRCFLFPCQAAIHONWADEVLYLNKFPDNGKSVGR 180
Db 121 ELSWAFRTTGGKYKPKFVSRRCFLFPCQAAIHONWADEVLYLNKFPDNGKSVGR 180

Qy 181 NDKSNHNLVVTETDRSTPKGKEYIEDDDTFEVLMTPELDEPCAFKVCPEASTTALVE 240
Db 181 NDKSNHNLVVTETDRSTPKGKEYIEDDDTFEVLMTPELDEPCAFKVCPEASTTALVE 240

Qy 241 PNEDKGHNLYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSNNMILAEKYITL 300
Db 241 PNEDKGHNLYQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSNNMILAEKYITL 300

Qy 301 HVTPEKGWSYASFSNIPVDFISQGDNDLVLLHILNVFPREFSMFTFTKYNQNSFQ 360
Db 301 HVTPEKGWSYASFSNIPVDFISQGDNDLVLLHILNVFPREFSMFTFTKYNQNSFQ 360

Qy 361 KLLSINESLPDYIKLDKIVYDLDYHLFYMKLQKKI 396
Db 361 KLLSINESLPDYIKLDKIVYDLDYHLFYMKLQKKI 396

RESULT 2
DCRTDM
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: JQ0439; B31786; F51487; A47002
R;Pulkka, A.; Keraenen, M.R.; Salmela, A.; Salmikangas, P.; Ihalaenen, R.; Pajunen, A.
Gene 86, 193-199, 1990
A;Title: Nucleotide sequence of rat S-adenosylmethionine decarboxylase cDNA: comparison
A;Reference number: JQ0439; MUID:90215298; PMID:2323572
A;Accession: JQ0439
A;Molecule type: mRNA
A;Residues: 1-333 <PUL>
A;Cross-references: UNIPROT:P17708; GB:M34464; NID:g202754; PIDN:AAA40683.1; PID:g202755
R;Pajunen, A.; Crozat, A.; Jaenne, O.A.; Ihalaenen, R.; Laitinen, P.H.; Stanley, B.; Mad
J. Biol. Chem. 263, 17040-17049, 1988
A;Title: Structure and regulation of mammalian S-adenosylmethionine decarboxylase.
A;Reference number: A92685; MUID:89034205; PMID:2460457
A;Accession: B31786
A;Molecule type: mRNA
A;Residues: 1-4, 'P', 6-145, 'A', 147-333 <PAJ>
A;Cross-references: GB:M34464
R;Pulkka, A.; Ihalaenen, R.; Aatsinki, J.; Pajunen, A.
FEBS Lett. 291, 289-295, 1991
A;Title: Structure and organization of the gene encoding rat S-adenosylmethionine decarboxylase
A;Reference number: S18487; MUID:92038054; PMID:1936275
A;Accession: S18487
A;Status: translation not shown

A;Molecule type: DNA
A;Residues: 1-145, 'A', 147-333 <PU2>
A;Cross-references: GB:M64274; NID:g206843; PIDN:AAA42105.1; PID:g206844
R;Pulkka, A.; Ihalaenen, R.; Suorsa, A.; Riviere, M.; Szpirer, J.; Pajunen, A.
Genomics 16, 342-349, 1993
A;Title: Structures and chromosomal localizations of two rat genes encoding S-adenosylme
A;Reference number: A47002; MUID:93300506; PMID:8314573
A;Accession: A47002
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-145, 'A', 147-333 <RES>
A;Cross-references: EMBL:Z15109; NID:g55705; PIDN:CAA78814.1; PID:g818018
C;Comment: The proenzyme is cleaved after translation into an alpha chain and a beta cha
quired for enzyme activity. The active enzyme catalyzes the decarboxylation of S-adenos
C;Comment: This is a key enzyme in the biosynthesis of polyamine.
C;Genetics:

A;Gene: AMD1B
A;Introns: 37/2; 66/2; 108/3; 143/1; 157/2; 236/3; 288/3
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase; polyamine biosynthesis
F;1-67/Domain: alpha chain #status predicted <CHA>
F;1-67,68-333/Product: adenosylmethionine decarboxylase #status predicted <MAT>
F;68-333/Domain: beta chain #status predicted <CHB>
F;68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 22.6%; Score 479; DB 1; Length 333;
Best Local Similarity 30.9%; Pred. No. 5e-29; Indels 56; Gaps 10;
Matches 117; Conservative 68; Mismatches 138; Indels 56; Gaps 10;

Qy 22 LDSTAFEGPEKLEIWFPPHKKSIITTEKTLNIGMDRWIEILKLVKCVLSMKTKEK 80
Db 1 MEAAHFEGETKLELVFWSRQSDASQSGDLATIPRSEWDVLLKDVQCSIIISVTKTDQ 60

Qy 81 DAPLSESSLFVFDHKLTKTCTTTTLFCLEKLFQIVEQELSWAFRTTGGKYKPF--- 137
Db 61 EAVLVSESSMFVSRKRRFILKTCGTCTLLKALVPLLLARD-----YSGFDSI 107

Qy 138 -KVFSRRCFLEPCQAAIHONWADEVLYLNKFPDNGKSVSGRDNKSNHNLVVTETDR 196
Db 108 QSFYRKNFMKPSHQGYPHRNFQSEIEFLNALFPNGAGYCMGRMN-SDCWYLYTLDLPE 166

Qy 197 STPKGKEYIEDDDTFEVLMTPELDEPCAFKVCPEASTTALVEPNEDKGHNLYQMTKN 256
Db 167 S-----RVINQPDQTLLELMSLDPAVMDQFYM-----KQGVAKDVTR 206

Qy 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSNNMILAEKYITLHVTPEKGWSYASFSN 316
Db 207 SGIRDLIPGSVIDATL-----FNPCGYSMNMGKSDGTWTHTITPEPEFSYVSEFN 258

Qy 317 IPVFDISQGDNDLVLLHILNVFPREFSMFTFTKYNQNSFQKLLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVVVEFKGKFTVTLFVN--QSSKRTVLSSPQKIDGFKRLD 309

Qy 377 KIVYDLDYHLFYMKLQKKI 395
Db 310 CQSAMFNDYNFVFTSPAKK 328

RESULT 3
DCHYDM
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: S22358; S19871
R;Tekwani, B.L.; Stanley, B.A.; Pegg, A.E.
Biochim. Biophys. Acta 1130, 221-223, 1992
A;Title: Nucleotide sequence of hamster S-adenosylmethionine decarboxylase cDNA.
A;Reference number: S22358; MUID:92223099; PMID:1562599
A;Accession: S22358
A;Molecule type: mRNA
A;Residues: 1-334 <TEK>
A;Cross-references: UNIPROT:P28918; EMBL:X63861; NID:g55521; PIDN:CAA45343.1; PID:g55522
A;Experimental source: liver of Syrian golden hamster

[illegible]

2

[illegible]

Db 11 FECTKLELWFQQDAS-KSGDLRDIRPFEDKLELVHCLLIISVTKDKQEAIVLSE 69

QY 88 SSLEFVHDHKLTKMTCTGTTTTLFCLEKLFQIVQEQLSWAFRTTGGKYKPP-----KVIFYSR 143

Db 70 SSMFVSKRRFILKCTGTTLLQALVPLELARE-----YCGFDGIGNFYFR 116

QY 144 RCLFPCQKQAAIHONNADEVLYLNFQDNGKSYSGRNDKSNHNLVYVTTDTRSTPKGKE 203

Db 117 KNFMKNHQYPRHNEHEVEFLQJLFPNGAAVCMGRIN-SDCWYLYTLDP-----DE 169

QY 204 Y-IEDDETPEVLMTLDPSCASKFVCGPEASTTALVEPNEDKGNLGYQMTNKLRLDEI 262

Db 170 YVLSQPDQTLLEILMSLDPVMDQF-----YMKEGVTANDVT 206

QY 263 YNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYTYTLHVTPEKGSYASFPESNIPV--F 320

Db 207 RVSGIRDLTGVSIDATMFSPCGSYMNGKSDGTWTIHTITPEPFSYNSFETNLSLTY 266

QY 321 DISQKODNLDVLLHLNVFQPREFSMTFTKYNQNSQFQKLKLSINESLPDYIKLDKIVY 380

Db 267 D-----DLISKVDVDFPKRKFVTTLFVN--QSSKCRVTLASQKIEGFKRLD 315

QY 381.DLDDYHLFYMKLOK 394

Db 316 QFNDFNFVFTSFAK 329

RESULT 6

DCUHDM

adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - human

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C;Accession: A31786

R;Pajunen, A.; Crozat, A.; Jaenne, O.A.; Ihalaenen, R.; Laitinen, P.H.; Stanley, B.; Mad J. Biol. Chem. 263, 17040-17049, 1988

A;Title: Structure and regulation of mammalian S-adenosylmethionine decarboxylase.

A;Reference number: A92685; MUID:89034205; PMID:2460457

A;Accession: A31786

A;Molecule type: mRNA

A;Residues: 1-334 <PAJ>

A;Cross-references: UNIPROT:P17707; GB:M34464

C;Comment: The proenzyme is cleaved after translation into an alpha chain and a beta chain required for enzyme activity. The active enzyme catalyzes the decarboxylation of S-adenosylmethionine.

C;Genetics:

A;Gene: GDB:AMD1

A;Cross-references: GDB:119674; OMIM:180980

A;Map position: 6pter-6qter

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase; polyamine biosynthesis

F;1-67/Domain: alpha chain #status predicted <CHA>

F;1-67,68-334/Product: adenosylmethionine decarboxylase #status predicted <MAT>

F;68-334/Domain: beta chain #status predicted <CHB>

F;68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 22.2%; Score 470; DB 1; Length 334;

Best Local Similarity 30.3%; Pred. No. 2.4e-28;

Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLNIGMDRWIEILKLVCKEVLSSMKTKEL 80

Db 1 MEAAHFEGETEKLELVFWSFQQPDANGSGDLATIPRSEWDILKQVCSIIISVTKDKQ 60

QY 81 DAFLLSESLFVFDHKLTKMTCTGTTTTLFCLEKLFQIVQEQLSWAFRTTGGKYKPP--- 137

Db 61 EAYVLSSESSFVSKRRFILKCTGTTLLKALVPLELARD-----YSGFDSI 107

QY 138 -KVIFYSRRCFLFPCQKQAAIHONNADEVLYLNFQDNGKSYSGRNDKSNHNLVYVTTDTR 196

Db 108 QSPFYGRKNFMKWSHOGYPHRNFQEEIEFLNALIPNGAGYCMGRIN-SDCWYLYTLDPPE 166

QY 197 STPKGKEYIBDDDETPEVLMTLDPSCASKFVCGPEASTTALVEPNEDKGNLGYQMTKN 256

Db 167 S-----RVISQPDQTLLEILMSLDPVMDQFYM-----KGVTAQDVRE 206

QY 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYTYTLHVTPEKGSYASFPESN 316

Db 207 SGIRDLTGVSIDATMFSPCGSYMNGKSDGTWTIHTITPEPFSYNSFETNLSLTY 258

QY 317 IPVFDISQKODNLDVLLHLNVFQPREFSMTFTKYNQNSQFQKLKLSINESLPDYIKLD 376

Db 259 -----LSQTSYD--DLIRKVVVEFKGKFTTILFVN--QSSKCRVTLASQKIEGFKRLD 309

QY 377 KIVYDLDYHLFYMKLOK 395

Db 310 CQSAMFNDFNFVFTSFAK 328

RESULT 7

T22361

adenosylmethionine decarboxylase (EC 4.1.1.50) precursor [validated] - Caenorhabditis el;

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T22361; T27363; T43626; T43521

R;White, S.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z19553

A;Accession: T22361

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-368 <WIL>

A;Cross-references: UNIPROT:O02655; EMBL:Z29171; PIDN:CA16315.1; GSPDB:GN00019; CESP:F4

A;Experimental source: clone F47G4

R;McLay, K.

submitted to the EMBL Data Library, June 1998

A;Reference number: Z20356

A;Accession: T27363

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-368 <W12>

A;Cross-references: EMBL:AL023853; PIDN:CAA19560.1; GSPDB:GN00019; CESP:F47G4.7

A;Experimental source: clone Y71A12C

R;Da'ara, A.A.; Walter, R.D.

Biochem. J. 336, 545-550, 1998

A;Title: Molecular and biochemical characterization of S-adenosylmethionine decarboxylase living nematode Caenorhabditis elegans.living nematode Caenorhabditis elegans.

A;Reference number: Z22535; MUID:99059682; PMID:9841864

A;Accession: T43626

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-368 <DAD>

A;Cross-references: EMBL:Y12499; PIDN:CAA73101.1

A;Accession: T43521

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-368 <DA2>

A;Cross-references: EMBL:Y12500; PIDN:CAA73102.1

C;Genetics:

A;Gene: samdc; F47G4.7 -

A;Map position: 1

A;Introns: 221/3; 294/2; 337/3

C;Function:

A;Description: EC 4.1.1.50 [validated, MUID:99059682]

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase

F;83/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 20.5%; Score 434; DB 2; Length 368;

Best Local Similarity 30.9%; Pred. No. 1.5e-25;

Matches 125; Conservative 72; Mismatches 129; Indels 78; Gaps 16;

QY 9 TNNHYDHELHLSATLSDTDAFEGPEKLEIWFPHKKSITT-EKTLNIGMDRWIEILKLVK 68

Db 7 TNFAVOTHVPKAP-DBEYFEGAEKLELWFCSTQNET--RSIRIPREIDAMLDIAR 63

QY 69 CEVLSSMKTKELDAFLLSSESLFVFDHKLTKMTCTGTTTTLFCLEKLFQIVQEQLSWAFRT 128

1990

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 18.8%; Score 398.5; DB 2; Length 357;
Best Local Similarity 33.0%; Pred. No. 7.5e-23;
Matches 121; Conservative 65; Mismatches 122; Indels 59; Gaps 16;

QY 24 STDAFEGPEKLLBIWPPPHKKSITTE---KTLRNIGMDRWIEILKLVKCEVLSMKTKEL 80
DB 6 SAIGFEGYERLEISFP--ESSFPADPDGKGLALNKSQIDEILEPAECTIVDSLNSQYL 63
QY 81 DAFLLSESLFVFDHKLTKMTCTGTTTLFLCKELFOIVEQELSWAFRTTGGKYKPKVF 140
DB 64 DSVLSESLFVVPYKIIKTCTGTTKLLSIPAILKAE-SLSLSVR-----NVK 112
QY 141 YSRCLFPCKQAATHQNADEVDYLNKFFD----NGKSYSVGRNDKSNHNLVYTTETDR 196
DB 113 YTRGSFIFFCAQSPHRSFSEVEILLDNYFGKLGLESNAFIMGNDPQPKWHVY----- 166
QY 197 STPKGKEYIEDDETFEVLMTLDPCEKASFCVCGPEASTTALVPEPNEDKGNHLYQMTKN 256
DB 167 SASVGSEQSDPTTYLTCMTGTDREKASVYF-KSESSAAL-----MTTR 211
QY 257 TRLDETYVNSAQSDLSFHDAFAFTPCGYSSNMILAEKYYITLHVTPKGGWYASFPESN 316
DB 212 SGTRKI-----LPSEIC---DEFPDPCGYSMNSI-EAAISITHVTPEDGFYASFEA- 261
QY 317 IPVFDISQGGQDNLDVLL-HILNVQFPRFSMTFTFTKNYQNSQFQKLLSINESLPDIYKL 375
DB 262 -AGYDL---KAQNLGMWIERVACLPQSPFSVAVHC-DVTCSEKLEQICSL--ELKEYSLD 314
QY 376 DKIVYDL 382
DB 315 EKINEEL 321

RESULT 11
T10750
probable adenosylmethionine decarboxylase (EC 4.1.1.50) - leaf mustard
C;Species: Brassica juncea (leaf mustard)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10750
R;Lee, T.; Liu, J.J.; Pua, B.C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17116
A;Accession: T10750
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <LEE>
A;Cross-references: UNIPROT:O49972; EMBL:U80916; NID:g2662405; PID:g2662406
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 18.3%; Score 387; DB 2; Length 369;
Best Local Similarity 31.4%; Pred. No. 5.9e-22;
Matches 116; Conservative 60; Mismatches 126; Indels 68; Gaps 13;

QY 24 STDAFEGPEKLLBIWPPPHKKSITTE-KTLRNIGMDRWIEILKLVKCEVLSMKTKELDA 82
DB 4 SAIGFEGYERLEISFPFVDTGCKGLRALPKSQIDILAPAECTIVSSLSNDELDS 63
QY 83 FLISESSLFVFDHKLTKMTCTGTTTLFLCKELFOIVEQELSWAFRTTGGKYKPKVYS 142
DB 64 YVLSSESLFIFPKYKIIKTCTGTTKLLSIPAILKLA-GELSLEVK-----VRYT 112
QY 143 RRCFLPCKQAATHQNADEVDYLNKFFD----NGKSYSVGRNDKSNHNLVYTTETDRST 198
DB 113 RGSFLCPGCGFPFHRFSFSEVLDGHFAKGLSSVAYLMDGDDDETCKWHVYASAPARN 172
QY 199 PKGKEYIEDDETFEVLMTLDPCEKASFCVCGPEASTTALVPEPNEDKGNHLYQMTKNTR 258
DB 199 PKGKEYIEDDETFEVLMTLDPCEKASFCVCGPEASTTALVPEPNEDKGNHLYQMTKNTR 258

DB 173 GNGNN--NNVYTEMCTGLDKKASVFKNESSAGS-----MTDNGS 215
QY 259 LDRIYVNSAQSDLSFHDAFAFTPCGYSSNMILAEKYYITLHVTPKGGWYASFPES--- 315
DB 216 IRKILFQS-QICD-----FEPECGYSWNSVEGDA-ISTIHVTPEDGFSYASFEAVGY 266
QY 316 NIPVFDISQGGQDNLDVLLHILNVQFPRFSMTFTFTKNYQNSQFQKLLSINESLPDIYKL 375
DB 267 DFTMDLSH-----LVSKVLTCFEPKQFSVAVHSSVAQ-KSYDSGLSV----- 308
QY 376 DKIVYDLDDY 385
DB 309 -----DLEDY 313

RESULT 12
S69191
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - wild barley
C;Species: Hordeum chilense (wild barley)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69191
R;Bresselhaus, T.; Barcelo, P.; Hagel, C.; Loez, H.; Humbeck, K.
Plant Mol. Biol. 30, 1021-1033, 1996
A;Title: Isolation and characterization of a Tritordeum cDNA encoding S-adenosylmethionine
A;Reference number: S69191; MUID:96270379; PMID:8639739
A;Accession: S69191
A;Molecule type: mRNA
A;Residues: 1-393 <DRE>
A;Cross-references: UNIPROT:Q42829; EMBL:X83881; NID:g1403043; PIDN:CAA58762.1; PID:g1403043
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted
F;72-393/Product: adenosylmethionine decarboxylase alpha chain #status predicted <MAT1>
F;247-262/Region: PEST sequence
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 17.8%; Score 378; DB 2; Length 393;
Best Local Similarity 30.4%; Pred. No. 3.1e-21;
Matches 116; Conservative 55; Mismatches 122; Indels 88; Gaps 16;

QY 24 STDAFEGPEKLLBIWFF-----PHKKSITTEKTLRNIGMDRWIEILKLVKCEVLSMKK 76
DB 6 SAIGFEGYERLEISFPFADPHRG-----LRALSRAQIDSVLDLARTIVSELS 59
QY 77 TKELDAFLSESLFVFDHKLTKMTCTGTTTLFLCKELFOIVEQELSWAFRTTGGKYK 136
DB 60 NKDFDSYVLSSESLFISQKIVIKTCGTMTLLTIPRIEELAE-ELCMPLAA----- 110
QY 137 FKVFYSRRRCFLFPCKQAATHQNADEVDYLNKFF-----DNGKSYSVGRNDK-SNHNLVY 191
DB 111 --VKYSGMFIFFCAQAPAPHRSPSEVDVNLRYFCHLNSGNAYVICDPAPKQKWHIYY 168
QY 192 TETDRSTPKGKEYIEDDETFEVLMTLDPCEKASFCVCGPEASTTALVPEPNEDKGNHLYG 251
DB 169 -----ATEQEPQPMVTLEMCMTGLDKTKASVFF-----KTHADGH 203
QY 252 -----QMTKNTRLDRIYVNSAQSDLSFHDAFAFTPCGYSSNMILAEKYYITLHVTPK 306
DB 204 VSCAKEMTKLSGISDI-IPMEVCD-----FDFPCGYSMNAINGSA-FSTIHVTPED 254
QY 307 GWSYASFE-SNIPVFDISQGGQDNLDVLLHILNVQFPRFS---MTFTKNYQNSQFQKLL 363
DB 255 GFSYASFEVQGMDSALAYG-----DIVKRVLCFCGSPSESVAVTIFGGRGHAATWCK-- 307
QY 364 SINESLPDIYKLDKIVYDLDD 384
DB 308 -----KLDAEAYDCNN 318

RESULT 13
T10707
adenosylmethionine decarboxylase (EC 4.1.1.50) 1 - clove pink
N;Alternate names: S-adenosylmethionine decarboxylase 1

C;Species: *Dianthus caryophyllus* (clove pink)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10787
 R;Lee, M.M.; Lee, S.H.; Park, K.Y.
 submitted to the EMBL Data Library, October 1995
 A;Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase
 A;Reference number: Z17089
 A;Accession: T10787
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-381 <LEE>
 A;Cross-references: UNIPROT:Q39676; EMBL:U38526; NID:g1155239; PID:g1155240
 A;Experimental source: cv. White Sim; carnation petal
 R;Kim, Y.J.; Lee, M.M.; Chang, K.S.; Lee, S.H.; Park, K.Y.
 submitted to the EMBL Data Library, March 1997
 A;Reference number: Z17144
 A;Accession: T10787
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-381 <KIM>
 A;Cross-references: EMBL:U94786; NID:g2406584; PID:g2406585
 A;Experimental source: strain White sim
 C;Genetics:
 A;Gene: Gcdcs9
 C;Function:
 A;Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (S)-deoxy-5-adenosylmethionine
 A;Pathway: polyamine biosynthesis
 C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
 C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
 F;93/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 17.8%; Score 376.5; DB 2; Length 381;
 Best Local Similarity 31.2%; Pred. No. 3.9e-21;
 Matches 112; Conservative 57; Mismatches 123; Indels 67; Gaps 11;

QY 5 IKELTNNY-----IDHLSATLSDTAFEGPEKLLIWIWPPPHKKSTTTE-KTLRNI 55
 DB 3 VPTLGSNNYNTVSPMGDDNNTWAL--SAIGFEGFEKRLRLEISFPFPGIFVDPEGKGLRAL 60
 QY 56 GMDRWIELKLVKEVLSMKKTKELDAFLSSESLFVDFHKLTKTKTCTTTTLFCLSKLFOIVQBSLSWA 115
 DB 61 SKQLDELILGPAECTIVDSLANESVDSVLSSESLFYPLKIVIKTCTGTTKLLTIPRIELELAB-ELSM 120
 QY 116 QIVEQELSWAFRTTQGGKYPKFFVYSRRCLFPCKQAAIHQNWADVDVYLNKFFDN--- 172
 DB 121 TLAD-----GLCLDVKSRYRTGRSFIFFGAQSYPHRSFSEVAVLKDYFNGLT 169
 QY 173 -GKSYSVGRNDKSNHWNLYTETDRSTPKGKEYIEDDDTFFVLMTELDPECAKFKVCGP 231
 DB 170 GSKAFVNGSPAKPKQKHVYSATAEPS-----YDDPVYTLMECMTGLDKGKASVFPKSE 222
 QY 232 EASTTALVEPNEKGNLNGVQMTKNTLDEIYVNSAQDSDLSPHDDAFATPCGYSNNMI 291
 DB 223 SASAAV-----MTETSGIRKLIPDSATCD-----FDPECGYSNNAI 259
 QY 292 LAEKYYVTLHVTPEKGSYASPFES--NIPVFDISQKQDNLDVLLHILNVFQPREPSM 347
 DB 260 EGPA-VSTIHTPEDGFSYASPEAVGVYDLKIVDNQ-----LVERVLCFQPREPSI 310

RESULT 14
 T03947
 adenosylmethionine decarboxylase (EC 4.1.1.50) - maize
 N;Alternate names: S-adenosylmethionine decarboxylase
 C;Species: *Zea mays* (maize)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T03947
 R;Michael, A.J.
 submitted to the EMBL Data Library, September 1996
 A;Reference number: Z15155
 A;Accession: T03947
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA

A;Residues: 1-400 <MIC>
 A;Cross-references: UNIPROT:O24575; EMBL:Y07767; PIDN:CAA69075.1
 C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
 C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
 F;78/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 17.6%; Score 372.5; DB 2; Length 400;
 Best Local Similarity 31.3%; Pred. No. 8.3e-21;
 Matches 109; Conservative 53; Mismatches 115; Indels 71; Gaps 14;

QY 20 ATLDSTDA-----PEGPEKLLIWIWPP-----PHKKSITTEKTLNIGMDRWIELK 65
 DB 2 AVLSAADASPVSAIGFEGYEKRLIETFSAPVFPVDPHGRG-----LRALSRAQIDSVLD 55
 QY 66 LVRCEVLSMKKTKELDAFLSSESLFVDFHKLTKTKTCTTTTLFCLSKLFOIVQBSLSWA 125
 DB 56 LARCTIVSELSNKPDSVLSSESLFYPLKIVIKTCTGTTKLLTIPRIELELAB-ELSM 114
 QY 126 FRTTQGGKYPKFFVYSRRCLFPCKQAAIHQNWADVDVYLNKFF-----DNKSYSVGRN 181
 DB 115 LAA-----VKYSRGTFFFGAQPAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDP 164
 QY 182 DK-SNHNWLYVTETDRSTPKGKEYIEDDDTFFVLMTELDPECAKFKVCGPEASTTALVE 240
 DB 165 ARPEQKWHVY-----ATEYEPQPMVYNLEMCMTGLDKKACVF-----FK 204
 QY 241 PNEDKGNLNGVQMTKNTLDEIYVNSAQDSDLSPHDDAFATPCGYSNNMILAEKYVTL 300
 DB 205 TNADGNTTCAKEMTKLSGISEI-IPWEICD-----FDPECGYSNNAIHGSA-FSTI 255
 QY 301 HVTPEKGSYASPFES-SNIPVFDISQKQDNLDVLLHILNVFQPREPSM 347
 DB 256 HVTPEKGSYASPEVVMGLDATALSYG-----DLVKRVLCRFGPSEPSV 298

RESULT 15
 T01934
 adenosylmethionine decarboxylase (EC 4.1.1.50) - common tobacco
 C;Species: *Nicotiana tabacum* (common tobacco)
 C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
 C;Accession: T01934
 R;Paramale, S.R.; Ernst, S.G.
 submitted to the EMBL Data Library, November 1997
 A;Reference number: Z14462
 A;Accession: T01934
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-361 <PAR>
 A;Cross-references: UNIPROT:O04009; EMBL:AF033100; NID:g2687583; PID:g2687584
 C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
 C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
 F;73/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 16.9%; Score 359; DB 2; Length 361;
 Best Local Similarity 33.8%; Pred. No. 7.8e-20;
 Matches 113; Conservative 50; Mismatches 121; Indels 50; Gaps 12;

QY 19 SATLDSTDAPEGPEKLLIWIWPP-PHKKSITTEKTLNIGMDRWIELKLVKEVLSMKKT 77
 DB 3 SALPVSAIGFEGPEKRLIETFSFPFGLFADPNGLKSLSKAQDLDEILGPAECTIVDSLSN 62
 QY 78 KELDAFLSSESLFVDFHKLTKTKTCTTTTLFCLSKLFOIVQBSLSWAFTTQGGKYPK 137
 DB 63 DDVDSVLSSESLFVYSYKIIKTKTCTGTTKLLAIPPLIKLAE-TLS-----LKQV 111
 QY 138 KVPYSRRCLFPCKQAAIHQNWADVDVYLNKFFD-----NGKSYSVGRNDKSNHWNLYVTE 193
 DB 112 DVRYTRGSFIFFGAQSPFPHRFSFSEVAVLVDGYFKLAAGSKAVIMGSPDKAQKWHVY--- 168
 QY 194 TDRSTPKGKEYIEDDDTFFVLMTELDPECAKFKVCGPEASTTALVEPNEKGNLNGVQ 253
 DB 169 ---SASAGPIQSNDPVYTLMECMTGLDREKASVYF-KTEGSSAA-----HM 210

Qy	254	TKNRLDEIYVNSAQDSDLSEHHDAPAF	PCGYSSNMILA	EKYVYTLHVTPEK	GSYASF	313
Db	211	TVRSGIRKILPNS-EICD-----	FEFPCGYSMNSIEGAA-LSTIHITPEDGFSYASF	261		
Qy	314	ESNIPVFDISQKQDNLDVLLHILNVFQPREFSM	347			
Db	262	EA--VGYDMKTMKLGPL--	VERVLACFPDDEFSI	291		

Search completed: May 11, 2005, 22:59:04
Job time : 23.0928 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:38:57 ; Search time 93.5567 Seconds
(without alignments)
2167.492 Million cell updates/sec

Title: US-10-732-923-406
Perfect score: 2118
Sequence: 1 MTVTIKELTNHNYIDHELSEA.....KIVYDLDDYHLYFMKLQKKI 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118	100.0	396	1	DCAM_YEAST
2	1377	65.0	406	2	Q6F855
3	1161.5	54.8	394	2	Q75284
4	955	45.1	367	2	Q6CT94
5	890.5	42.0	434	2	Q6BPN1
6	756	35.7	418	2	Q6C579
7	681	32.2	503	2	Q9Y7F3
8	571	27.0	378	1	DCAM_SCHPO
9	480	22.7	333	1	DCAM_RAT
10	479	22.6	334	1	DCAM_MESAU
11	479	22.6	334	1	DCM1_MOUSE
12	478	22.6	334	1	DCM2_MOUSE
13	478	22.6	334	1	DCM2_MUASP
14	476	22.5	335	1	DCAM_XENLA
15	473	22.3	334	1	DCAM_BOVIN
16	471.5	22.3	385	2	Q8TLE3
17	471	22.2	347	1	DCAM_DROME
18	470	22.2	334	1	DCAM_HUMAN
19	466	22.0	334	2	Q6N0B2
20	462	21.8	334	2	Q7ZVU7
21	444	21.0	338	2	Q7Q1V3
22	442.5	20.9	365	1	DCAM_ONCVO
23	434	20.5	368	1	DCAM_CAEEL
24	419.5	19.8	335	2	Q9BLJ5
25	404	19.1	362	1	DCAM_ARATH
26	401.5	19.0	353	1	DCAM_PEA
27	398.5	18.8	357	1	DCAM_CATRO
28	397.5	18.8	353	1	DCAM_VICFA
29	387	18.3	369	1	DCA2_BRAJU
30	387	18.3	369	2	Q6S2S4
31	384	18.1	367	1	DCA3_BRAJU

32	383.5	18.1	358	2	Q852S9
33	383	18.1	361	2	Q6RUQ3
34	381	18.0	361	1	DCAM_DAUCA
35	378	17.8	393	1	DCAM_HORCH
36	376.5	17.8	381	1	DCAM_DIACA
37	376	17.8	392	2	Q9ZFU1
38	375.5	17.7	366	1	DCAM_ARATH
39	375.5	17.7	366	2	Q94Q05
40	375.5	17.7	366	2	Q6QJ69
41	374.5	17.7	362	1	DCAM_IPONI
42	374	17.7	370	2	Q84LA2
43	372.5	17.6	400	1	DCAM_MAIZE
44	368.5	17.4	362	1	DCAM_IPOBA
45	368.5	17.4	368	1	DCA1_BRAJU

ALIGNMENTS

RESULT 1
ID DCAM_YEAST STANDARD; PRT; 396 AA.
AC P21182;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SAMDC) (Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain).
DE Name=SP22; OrderedLocNames=YOL052C; ORFNames=O1275;
GN Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91093074; PubMed=2266128;
RA Kashiwagi K., Taneja S.K., Liu T.-Y., Tabor C.W., Tabor H.;
RT "Spermidine biosynthesis in Saccharomyces cerevisiae. Biosynthesis and processing of a proenzyme form of S-adenosylmethionine decarboxylase.";
RT J. Biol. Chem. 265:22321-22328(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / FY73;
DE MEDLINE=96381248; PubMed=8789261;
DOI=10.1002/(SICI)1097-0061(199601)12:1<67::AID-YEAS84>3.0.CO;2-F;
RA Mannhaupt G., Vetter I., Schwarlose C., Mittel S., Feldmann H.;
RT "Analysis of a 26 kb region on the left arm of yeast chromosome XV.";
RL Yeast 12:67-76(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Ansoerge W., Benes V., Rechmann S., Schwager C., Teodoru C., Voss H.,
Wiemann S.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: S-adenosylmethionine decarboxylase is essential for normal growth, sporulation, maintenance of ds-RNA virus, biosynthesis of spermine and spermidine.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
CC -!- COFACTOR: Pyruvoyl group.
CC -!- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
CC -!- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC -----
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CC

Q852S9	malus domes
Q6RUQ3	daucus caro
Q94X63	daucus caro
Q42829	hordeum chi
Q39676	dianthus ca
Q9ZPJ1	trititum ae
Q96286	arabidopsis
Q940G5	arabidopsis
Q6QJ69	brassica ju
Q96471	ipomeia nil
Q84LA2	narcissus p
Q24575	zea mays (m
Q9M6K1	ipomeia bat
Q42613	brassica ju

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CC -----
DR ENBL; M38434; AAA34421.1; --
DR ENBL; X91067; CAA62536.1; --
DR ENBL; Z74794; CAA99058.1; --
DR PIR; S12772; DCBYDM.
DR HSP; P17707; IJLO.
DR IntAct; P21182; --
DR GERMOnline; 143474; --
DR SGD; S000003412; SPE2.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IDA.
DR GO; GO:0015940; P:pantothenate biosynthesis; IMP.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 2.
DR TIGRFAMs; TIGR00535; SAM DCASE; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Direct protein sequencing; Lyase; Pyruvate;
KW Spermidine biosynthesis; Zymogen.
FT CHAIN 1 87 S-adenosylmethionine decarboxylase beta
FT CHAIN 88 396 chain.
FT CHAIN 88 396 S-adenosylmethionine decarboxylase alpha
FT SITE 87 88 chain.
FT MOD_RES 88 88 Cleavage (nonhydrolytic).
FT ACT_SITE 29 29 Pyruvic acid (Ser).
FT ACT_SITE 32 32 By similarity.
FT ACT_SITE 102 102 By similarity.
SQ SEQUENCE 396 AA; 46232 MW; 8B63676CB5636D71 CRC64;

Query Match 100.0%; Score 2118; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 6.5e-156;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVTIKELTNHNYIDHELSTLDSTDAFEGPEKLEIWFPPHKKSIITETLNIGMDRW 60
DB 1 MTVTIKELTNHNYIDHELSTLDSTDAFEGPEKLEIWFPPHKKSIITETLNIGMDRW 60
QY 61 IEILKLVKCEVLSMKTKELDALLSESLVFDPHKLTMKTCGTTTTLFCKLEKLFQIVEQ 120
DB 61 IEILKLVKCEVLSMKTKELDALLSESLVFDPHKLTMKTCGTTTTLFCKLEKLFQIVEQ 120
QY 121 ELSWAFRTTGGYKPKFVYSRRCFLFPCQAIIHQNWADVDYLNKFPDNGKSVGR 180
DB 121 ELSWAFRTTGGYKPKFVYSRRCFLFPCQAIIHQNWADVDYLNKFPDNGKSVGR 180
QY 181 NDKSNHNLVYTDRTSTPKGKEYIEDDDTFFVLMTLDPCEKSFVCGPEASTTALVE 240
DB 181 NDKSNHNLVYTDRTSTPKGKEYIEDDDTFFVLMTLDPCEKSFVCGPEASTTALVE 240
QY 241 PNEDKGHNLYGQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYTYTL 300
DB 241 PNEDKGHNLYGQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYTYTL 300
QY 301 HVTPEKGWSVASFESNIPVDISQGDNDLVLLHNLVQPREFTPTTKYQNSQFQ 360
DB 301 HVTPEKGWSVASFESNIPVDISQGDNDLVLLHNLVQPREFTPTTKYQNSQFQ 360
QY 361 KLLSINESLPDYIKLKIYVDLDDYHLFYMKLQKKI 396
DB 361 KLLSINESLPDYIKLKIYVDLDDYHLFYMKLQKKI 396

RESULT 2
Q6FS85 PRELIMINARY; PRT; 406 AA.
AC Q6FS85
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Candida glabrata strain CBS138 chromosome H complete sequence.
GN ORFNames=CAGL0H02607g;

```

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OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durzens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykaster C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
EMBL: CR380954; CAG59842.1; --
GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
GO; GO:0008295; P:spermidine biosynthesis; IEA.
GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR00504; RNA rec mot.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 2.
DR TIGRFAMs; TIGR00535; SAM DCASE; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
DR PROSITE; PS0030; RRM RNP 1; UNKNOWN 1.
DR PROSITE; PS0030; RRM RNP 1; UNKNOWN 1.
SQ SEQUENCE 406 AA; 47686 MW; E970993AFA7209BE CRC64;

Query Match 55.0%; Score 1377; DB 2; Length 406;
Best Local Similarity 52.4%; Pred. No. 2e-98;
Matches 254; Conservative 66; Mismatches 71; Indels 16; Gaps 5;

QY 1 MTVTIKELTNHNYIDHELSTLDSTDAFEGPEKLEIWFPPHKKSIITETLNIGMDRW 55
DB 1 MTVTIKELTNHNYIDHELSTLDSTDAFEGPEKLEIWFPPHKKSIITETLNIGMDRW 55
QY 56 GMDRWIEILKLVKCEVLSMKTKELDALLSESLVFDPHKLTMKTCGTTTTLFCKLEKLF 115
DB 56 GMDRWIEILKLVKCEVLSMKTKELDALLSESLVFDPHKLTMKTCGTTTTLFCKLEKLF 115
QY 61 AVEKVAAILKLVKCEVLSMKTKELDALLSESLVFDPHKLTMKTCGTTTTLFCKLEKLF 120
DB 61 AVEKVAAILKLVKCEVLSMKTKELDALLSESLVFDPHKLTMKTCGTTTTLFCKLEKLF 120
QY 116 QIVQEELSWAFRTTQGGYKPKFVYSRRCFLFPCQAIIHQNWADVDYLNKFPDNGKSVGR 172
DB 116 QIVQEELSWAFRTTQGGYKPKFVYSRRCFLFPCQAIIHQNWADVDYLNKFPDNGKSVGR 172
QY 121 RIVEEELGMDMRACKENGVKHPHVFYSRRCFLFPCQAIIHQNWADVDYLNKFPDNGKSVGR 180
DB 121 RIVEEELGMDMRACKENGVKHPHVFYSRRCFLFPCQAIIHQNWADVDYLNKFPDNGKSVGR 180
QY 173 GKSYSGRNDKSNHNLVYTDRTSTPKGKEYIEDDDTFFVLMTLDPCEKSFVCGPEASTTALVE 231
DB 173 GKSYSGRNDKSNHNLVYTDRTSTPKGKEYIEDDDTFFVLMTLDPCEKSFVCGPEASTTALVE 231
QY 181 GSYLVGRSDQSNHNLVYTDRTSTPKGKEYIEDDDTFFVLMTLDPCEKSFVCGPEASTTALVE 240
DB 181 GSYLVGRSDQSNHNLVYTDRTSTPKGKEYIEDDDTFFVLMTLDPCEKSFVCGPEASTTALVE 240
QY 232 EASTTALVE----PNEDKGHNLYGQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSS 287
DB 232 EASTTALVE----PNEDKGHNLYGQMTKNTRLDEIYVNSAQSDLSFHHDAFAFTPCGYSS 287
QY 241 EVKTVESQSDENTSDEGHLSGKMTNATRLDRVYNN---EKNVSFHHDAFAFTPCGYSS 297
DB 241 EVKTVESQSDENTSDEGHLSGKMTNATRLDRVYNN---EKNVSFHHDAFAFTPCGYSS 297
QY 288 SNMILAEKYTYTLHVTPEKGWSVASFESNIPVDISQGDNDLVLLHNLVQPREFTPTTKYQNSQF 347
DB 288 SNMILAEKYTYTLHVTPEKGWSVASFESNIPVDISQGDNDLVLLHNLVQPREFTPTTKYQNSQF 347
QY 298 SNIIMDEEYTYTLHVTPEKGWSVASFESNIPVDISQGDNDLVLLHNLVQPREFTPTTKYQNSQF 357
DB 298 SNIIMDEEYTYTLHVTPEKGWSVASFESNIPVDISQGDNDLVLLHNLVQPREFTPTTKYQNSQF 357
QY 348 TFFTKYQNSQFQKLLSINESLPDYIKLKIYVDLDDYHLFYMKLQKKI 394
DB 348 TFFTKYQNSQFQKLLSINESLPDYIKLKIYVDLDDYHLFYMKLQKKI 394
QY 358 TFFCKSMDSNFKLLMKTSGEINYYTKDRIIYDLDYHLLYIRFER 404
DB 358 TFFCKSMDSNFKLLMKTSGEINYYTKDRIIYDLDYHLLYIRFER 404

RESULT 3
Q75E84 PRELIMINARY; PRT; 394 AA.
ID Q75E84

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AC Q6BPN1;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Debaryomyces hansenii chromosome E of strain CBS767 of Debaryomyces
DE hansenii.
GN ORFNames=DEHA0E12826g;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=284592;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382137; CAG8078.1; -
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 2.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 434 AA; 49959 MW; 4282D7BF6CCBF209 CRC64;

Query Match 42.0%; Score 890.5; DB 2; Length 434;
Best Local Similarity 44.7%; Pred. No. 1.2e-60;
Matches 193; Conservative 64; Mismatches 114; Indels 61; Gaps 14;

QY 13 YIDHLSATLSDTDAFEGPEKLEIWFPPHKKSITTE-KTLRNIQMDRWIEILKLVKCEV 71
DB 11 YVDHLSANLSDTFAFEGPEKLEIWFPPHKKSITTEIPKKSEGLRSIPLEKQVRVLDVSK 70

QY 72 LSKMKTKELDAFLSSSLFVFDHKLTKMTCTGTTTLFLEKLFQIVEQELSWAFRTQ 131
DB 71 LSKMKSKFMDAYLLSSSLFVFPFKLILTKCTGTTTLACLESFETVQNVV-----EG 123

QY 132 ---GKYKPKFVYRRRCFLPCKQAATHQWAEVDVYLNKFFDNGKSYSGRNDKSNHN 188
DB 124 IDNFNVNFKIFVRSRSMFDPDKQKVRNWKQKEVLLNKNFYONGKSYIVGDTFGDDHWY 183

QY 189 LYVTEDTRSPKGEYIEDD--DETEVLMTLDPCEAKSFVCGPEASTTALV-----EP 241
DB 184 LYWGGRD-SVP-SDENANDNVROTPEILMTLNPEKAENFIADRKPGAESLKESEEE 241

QY 242 NEPKGNLGVQMTNTRLDIYNSAQ-----DSD----- 271
DB 242 EHLGHDGMGQTCWCKSKLSDIFPGSNKKLKHSLPSPSLSDSMELSDSDECLKETPTNSD 301

QY 272 -LSFPHDAFAFTPCGYSSNMILAEK--YYTTLHTVTPKSGWYSASFESNIPVFDISQKOD 328
DB 71 VLSMKTKTKELDAFLSSSLFVFDHKLTKMTCTGTTTLFLEKLFQIVEQELSWAFRTQ 130

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302 KPFKFIHDAFAFSPCGYSSNSISNNNGYYVTLHTPESGWSYASFETNYPF--TKDSNES 359
329 NLDVLLHILNVFQPRFMSMTFTKN---YQNSQFQKLLSNESLPD--YTKLQIVYDLD 383
360 IVDLANKVLDFQPGKFSVTFITESDTHDKFNFDLSNCAEDLSEQGQKQERVLVDLK 419
384 -DYHLFYMVKLOK 394
420 FGKLLYLNFVK 431

RESULT 6
Q6C579 PRELIMINARY; PRT; 418 AA.
AC Q6C579;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Similar to tr|Q9Y7F3 Neurospora crassa S-adenosylmethionine
DE decarboxylase.
GN ORFNames=YALI0E20361g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382131; CAG79778.1; -
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001220; Lectin_legB.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
DR PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
SQ SEQUENCE 418 AA; 46500 MW; 9469E694A6F01A5C CRC64;

Query Match 35.7%; Score 756; DB 2; Length 418;
Best Local Similarity 38.5%; Pred. No. 3e-50;
Matches 164; Conservative 68; Mismatches 126; Indels 68; Gaps 10;

QY 12 NYDHELSTLSDTDAFEGPEKLEIWFPPHKKSIT-TEXTLNIQMDRWIEILKLVKCE 70
DB 5 HYNHQAVIDLSDAFAFEGPEKLEIWFAPNQBSLEGTKSLRNVSVAQEQELNIVQCK 64

QY 71 VLSMKTKTKELDAFLSSSLFVFDHKLTKMTCTGTTTLFLEKLFQIVEQELSWAFRTQ 130

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Db 65 VLSSVHTSVLDAPVLSSESNFVPPHKLVLKCTGTTLLVGIPOKLBIA-----RTIA 116
QY 131 --CGKTKPKFVYSRCFLPPCKQAAHONWADEVDYLNKFFDNGKSYSGVRNDKSNHWN 188
Db 117 GFANATPRVVFVSHKTFNCFEQAQAPPHKSKWDEVSYLSQFNGKAYLVGDTTSDHHWY 176
QY 189 LYVTETD--RSTPKGKEY-IEDDETFEVLMTLDPCEASKFV----- 228
Db 177 CVYTGDDHEEVAHAKDHISSHDETWEILMTDLPSSAQOQFTDRLPGDANNAGFOHKQ 236
QY 229 -----CGPEASTTALVEPNEDKGNLYGQMTKTRLEIYV 264
Db 237 ELVGVHVVVKAETSDATSDSGATPACSGTCKADP-----GVLGAYVSTQSGIADIY 292
QY 265 NSAQDSDLSFHDHDAFAFTPCGYSSNMILAEKYTYTLHTVTPKGSVSPESNIPVFDISQ 324
Db 293 R-----NKASVAVDSFCTPCGYSAANAIVDSGYTYTHVTPQHCVSASFETNVPAYEG- 347
QY 325 GKDNLDVLHLNVQPREFSMTFTTKYQNSQFQKLLSINBSLPDYIKLDXIVYDLDD 384
Db 348 --MSNIDVIEKVLNVPRPKLSVTLF--EAENNSLQDCHQFARHLDGYKRTDKVLYEFDG 403
QY 385 YHLFYM 390
Db 404 YQMVYV 409

RESULT 7

Q9Y7F3 ID Q9Y7F3 PRELIMINARY; PRT; 503 AA.
AC Q9Y7F3; DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE S-adenosylmethionine decarboxylase (EC 4.1.1.50) (Spe-2).
GN Names=Spe-2; Synonyms=514A6.060;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309329; PubMed=10852489; DOI=10.1007/s004380051215;
RA Hoyt M.A., Williams-Abbott L.J., Pitkin J.W., Davis R.H.;
RT "Cloning and expression of the S-adenosylmethionine decarboxylase gene
of Neurospora crassa and processing of its product.";
RL Mol. Gen. Genet. 263:664-673 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF151380; AAD34030.1; -
DR EMBL; AL670007; CAD21308.1; -
DR HSSP; PL7707; 1JL0.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR00362; Fumarate_lyase.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 2.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
DR PROSITE; PS00163; FUMARATE_LYASES; UNKNOWN_1.
KW Lyase.
SQ SEQUENCE 503 AA; 54721 MW; 4EF83A7BAA2B407B CRC64;

Query Match 32.2%; Score 681; DB 2; Length 503;
Best Local Similarity 32.5%; Pred. No. 2.5e-44;
Matches 161; Conservative 85; Mismatches 128; Indels 122; Gaps 13;
QY 2 TWIKELTHNVYIDHLSATLSDAFEGPEKLELWFFPHKXSI---TTEKTLRIGMD 58
Db 14 TFSPESGTPLYLTINHVAADLSDTNAFEGPEKLELVFAPSAKALPAGVKEGGLKANPD 73
QY 59 RTEILKLVKCEVLSMKTKELDAPLSSSLFVDFHKLTMKTCGTTTLFCLKELPQIV 118
Db 74 SWTPMLDLVHCKVLSINSENVDSYLLSSSMVFPHKILKTCGTTLLGLDLMRIA 133
QY 119 EDELWAFRTQGGK-----YKPFKVYSRRCLFPCQAAIHONWADEVDYLNKFPDNG 173
Db 134 AVEAGPPFHNVASLEDPKVAATPLRVFYSKQNFLLFKQKQPHKSWRDEVTFLDNMPENG 193
QY 174 KSYSGVRNDKSNHNLVYTTEDRS-----TPKGKEYIED 207
Db 194 SAYMVGKMN-GDHWLYLYITPTSSLTPTPTSSRGVSPSRRSKIPTGIVAPFGVIENN 252
QY 208 DDETFEVLMTLDPCEASKFV-----CG----- 230
Db 253 ADETLEILMTDLDPENAKFPYLEEATAIAKELFKSEANGDASFDVFSSGDCDADGQA 312
QY 231 --PEASTTALVEPNEDKGNLYGQMTKTRLEIYVNSA-QSDLSLFFHDAFAFTPCGYS 287
Db 313 ILPEALT-----EGHALGTWVSEACGLSAVYPTSTVPDARI---DAYQFSPCGFS 360
QY 288 SNMIL-----AEKYTYTLHTVTPKGSVSPESNIPVFDISQKDNLDVLHLI 336
Db 361 ANGVPVPPVAGADGTIPKSGHYFTVHTVTPQCSFASFETNVPG---GQNGRQTAEVIEQV 417
QY 337 LNVFQPREFSMTFF-----TKYQNSQFQKLLSINBSLPDYIKLDKIV 379
Db 418 VNIFFRFSVILFEAKGALATTPGEDADDSRRSWGAAAKQRMERIN---GTRVDRIV 473
QY 380 YLDLDYHLYFMKLQKK 395
Db 474 HDPEDYDLVFRYVERE 489

RESULT 8

DCAM SCHPO ID DCAM SCHPO STANDARD; PRT; 378 AA.
AC Q9P7E3; DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SambDC) (Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain).
GN Name=spe2; ORFNames=SPBP4H10.05c;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21293067; PubMed=11859360; DOI=10.1074/jbc.M010643200;
RA Chattopadhyay M.K., Murakami Y., Matsufuji S.;
RT "Antizyme regulates the degradation of ornithine decarboxylase in
fission yeast Schizosaccharomyces pombe. Study in the spe2 knockout
strains.";
RL J. Biol. Chem. 276:21235-21241 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RESULT 10
DCAM MESAU

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Db 108 QSFYKRNKPKSHQYPRNFQEEIEFLNAPFGAAVCMGRMN-SDCWLYLTLDPE 166
Qy 197 STPKGKEYIEDDETPEVLMTLDPKCAKFKVCGPEASTTALVEPNEDKGNHLYQWTKN 256
Db 167 S-----RVINOPDOTLEILMSELDPAVMDQFYM-----KDGVTAKDVIRE 206
Qy 257 TRLDEIVNSAQSDLSFHHDAFAFPCCGSSNNMILAKEYYYTLHVTPEKWSYASPSN 316
Db 207 SGIRIDIPGSVIDATL-----FNPCGYSNMGMKSDGTWYTHITPEPEFSYVSEFN 258
Qy 317 IPVEDISQGDMLDLVLLHILNFPQPEFMTFTKYNQNSQKLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVEVFKPKGFVTLFVN--QSSKRTVLSSPKIEGFKRLD 309
Qy 377 KIYVDLDYHLFYMKLQK 395
Db 310 CQSAMENDYNFVFTSPAK 328

RESULT 11
ID DCMI_MOUSE STANDARD; PRT; 334 AA.
AC P31154;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme 1 (EC 4.1.1.50) (AdoMetDC
DE 1) (SamdC 1) (Contains: S-adenosylmethionine decarboxylase 1 alpha
DE chain; S-adenosylmethionine decarboxylase 1 beta chain).
GN Name=Amd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=93080592; PubMed=149493;
RA Waris T., Ihalaainen R., Keraenen M.-R., Pajunen A.;
RT "Molecular cloning of the mouse S-adenosylmethionine decarboxylase
RT cDNA: specific protein binding to the conserved region of the mRNA 5'-
RT untranslated region.";
RL Biochem. Biophys. Res. Commun. 189:424-429 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93345510; PubMed=8344293;
RA Suzuki T., Sadakata Y., Kashiwagi K., Hoshino K., Kakinuma Y.,
RA Shirahata A., Igarashi K.;
RT "Overproduction of S-adenosylmethionine decarboxylase in ethylglyoxal-
RT bis(guanylhydrazine)-resistant mouse FM3A cells.";
RL Eur. J. Biochem. 215:247-253 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Spleen;
RX MEDLINE=20035739; PubMed=10570962; DOI=10.1016/S0378-1119(99)00355-8;
RA Nishimura K., Kashiwagi K., Matsuda Y., Jaenne O.A., Igarashi K.;
RT "Gene structure and chromosomal localization of mouse S-
RT adenosylmethionine decarboxylase.";
RL Gene 238:343-350 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
CC adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -I- COFACTOR: Pyruvoyl group.
CC -I- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -I- SUBUNIT: Heterotetramer of two alpha and two beta chains (By
CC similarity).
CC -I- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z14986; CAA78710.1; -
DR EMBL; D12780; BAA02243.1; -
DR EMBL; AB025024; BAA83784.1; -
DR EMBL; BC011110; AAH110.1; -
DR HSP; P17707; IJEN.
DR MGD; MGI:88004; Amd1.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR Trifam; TRIG00535; SAM_DCase; 1.
DR TIGRfam; TIGR01336; ADOMETDC; 1.
KW Decarboxylase; lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 67
FT S-adenosylmethionine decarboxylase 1 beta
FT chain.
FT CHAIN 68 334
FT S-adenosylmethionine decarboxylase 1
FT alpha chain.
FT SITE 67 68
FT Cleavage (nonhydrolytic).
FT MOD_RES 68 68
FT Pyruvic acid (Ser).
FT ACT_SITE 8 8
FT By similarity.
FT ACT_SITE 11 11
FT By similarity.
FT ACT_SITE 82 82
FT By similarity.
SQ SEQUENCE 334 AA; 38272 MW; 7950A1E9A9ACBD72 CRC64;

Query Match 22.6%; Score 479; DB 1; Length 334;
Best Local Similarity 30.9%; Pred. No. 6.8e-29;
Matches 117; Conservative 69; Mismatches 137; Indels 56; Gaps 10;

Qy 22 LDSTDAPEGEKLEIWFPHKKSITT-EKTLNIGMDRWIEILKLVKCVLSNKKTKEL 80
Db 1 MEAAHFEETGKLELVNFRSQSDASQSGSDGLRTIPRSEWDVLKDVQCSIIISVTKDKQ 60
Qy 81 DAFILSSSLVFDHKLTMKTCGTTTLTFLCGLKFLQIVEQLSWAFRTTQGGKYKPF--- 137
Db 61 EAVLSESSMFWKRRFILTCTGTTLLKALVPLKLARD-----YSGFDSI 107
Qy 138 -KVYFRRRCFLFPCKAAIHQNWAEVDYLNKPFNDGKYSVGRNDSKNHNLVYTETR 196
Db 108 QSFYKRNKPKSHQYPRNFQEEIEFLNAPFGAAVCMGRMN-SDCWLYLTLDPE 166
Qy 197 STPKGKEYIEDDETPEVLMTLDPKCAKFKVCGPEASTTALVEPNEDKGNHLYQWTKN 256
Db 167 S-----RVISQPDQTLLEILMSELDPAVMDQFYM-----KDGVTAKDVIRE 206
Qy 257 TRLDEIVNSAQSDLSFHHDAFAFPCCGSSNNMILAKEYYYTLHVTPEKWSYASPSN 316
```


Db 207 SGIRDLIPGVIDATL-----FNPCGYSMGMKSDGTWYTHITPEPEFSVSPETN 258
 QY 317 IPVFDISQKQDNLVLLILNVPQREPSMTFTKYNQNSQKLLSINESLPDIYKLD 376
 Db 259 -----LSQTSYD--DLIRKVVVEFKPKGFVTTLVFN--QSSKCTVLSSPKQIDGFKRLD 309
 QY 377 KIVYDLDYHLFYMKLQKK 395
 Db 310 CQSAMFNDYNFVFTSPAKK 328

RESULT 12
 DCM2_MOUSE
 ID DCM2_MOUSE STANDARD; PRT; 334 AA.
 AC P82184;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme 2 (EC 4.1.1.50) (AdoMetDC
 2) (SamDC 2) [Contains: S-adenosylmethionine decarboxylase 2 alpha
 chain; S-adenosylmethionine decarboxylase 2 beta chain].
 GN Name=Amd2; Synonym=Amd-2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Spine;
 RX MEDLINE=95137575; PubMed=7890685; DOI=10.1074/jbc.270.10.5642;
 RA Persson K., Holm I., Heby O.;
 RT "Cloning and sequencing of an intronless mouse S-adenosylmethionine
 decarboxylase gene coding for a functional enzyme strongly expressed
 in the liver.";
 RL J. Biol. Chem. 270:5642-5648 (1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ILE-70.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98285531; PubMed=9620866;
 RA Nishimura K., Liisanantti M., Muta Y., Kashiwagi K., Shirahata A.,
 RA Janne M., Kankare K., Janne O.A., Igarashi K.;
 RT "Structure and activity of mouse S-adenosylmethionine decarboxylase
 gene promoters and properties of the encoded proteins.";
 RL Biochem. J. 332:651-659 (1998).
 CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
 adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -I- COFACTOR: Pyruvoyl group.
 CC -I- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
 aminopropyl moiety required for spermidine and spermine
 biosynthesis from putrescine.
 CC -I- SUBUNIT: Heterotetramer of two alpha and two beta chains (By
 similarity).
 CC -I- TISSUE SPECIFICITY: Widely expressed. Particularly abundant in
 liver.
 CC -I- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z23077; CAA80614.1; -;
 DR PIR; A55948; A55948.
 DR HSSP; P17707; I17B.
 DR MGD; MGI:133311; Amd2.
 DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IDA.
 DR InterPro; IPR001985; SAM_decarbox.
 DR Pfam; PF01536; SAM_decarbox; 1.
 DR ProDom; PD002379; SAM_decarbox; 1.

DR TIGRFAMS; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
 FT CHAIN 1 67 S-adenosylmethionine decarboxylase 2 beta
 FT CHAIN 68 334 chain.
 FT CHAIN 68 334 S-adenosylmethionine decarboxylase 2
 FT SITE 67 68 alpha chain.
 FT MOD_RES 68 68 Cleavage (nonhydrolytic).
 FT ACT_SITE 8 8 Pyruvic acid (Ser).
 FT ACT_SITE 11 11 By similarity.
 FT ACT_SITE 82 82 By similarity.
 FT ACT_SITE 70 70 By similarity.
 FT MUTAGEN I->M: Increases specific activity and
 proenzyme-processing activity.
 SQ SEQUENCE 334 AA; 38282 MW; A6DFE76F2FC8F4F4 CRC64;
 Query Match 22.6%; Score 478; DB 1; Length 334;
 Best Local Similarity 30.9%; Pred. No. 8.1e-29;
 Matches 117; Conservative 69; Mismatches 137; Indels 56; Gaps 10;
 QY 22 LDSTDAFEPGEKLEIWFPPHKKSIIT-EKTLRNIGMDRWIEILKLVKCEVLSMKTKEL 80
 Db 1 MEAAHFEGETEKLLEWVFSRQSDASQSGDLRTIPSEWDVLLKDVQCSIIIVTKDKQ 60
 QY 81 DAPLLSESLFVDPHKLTKWTCGTTTTLFCLEKLFQIVEQELSWAFRTTGGKYKPF--- 137
 Db 61 EAVVSESSIFVSKRRPILKTCGTTLLKALVPLLLARD-----YSGFDSI 107
 QY 138 -KVYSRRCLFPCKQAATHQWAEVDVYLKNEFDNGKSYSGRNDKSNHNLVYVTFDR 196
 Db 108 QSEFFSRKFMKPSHOGYFHRNFQIEFLNVPFNGAAYCMGRMN-SDCWLYTLDPPE 166
 QY 197 STPKGEYTEDDDTEFEVLMTLDPCCASKFVCGPEASTTALVEPNEDKGNLGYQMTKN 256
 Db 167 S-----RVISQPDQTLLEIMSELDPAVMDQFYM-----KGVTAQDVRE 206
 QY 257 TRLEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYYTLVHTVPEKWSVASPESN 316
 Db 207 SGIRDLIPGVIDATL-----FNPCGYSMGMKSDGTWYTHITPEPEFSVSPETN 258
 QY 317 IPVFDISQKQDNLVLLILNVPQREPSMTFTKYNQNSQKLLSINESLPDIYKLD 376
 Db 259 -----LSQTSYD--DLIRKVVVEFKPKGFVTTLVFN--QSSKCTVLSSPKQIDGFKRLD 309
 QY 377 KIVYDLDYHLFYMKLQKK 395
 Db 310 CQSAMFNDYNFVFTSPAKK 328

RESULT 13
 DCM2_MOUSE
 ID DCM2_MOUSE STANDARD; PRT; 334 AA.
 AC P82185;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme 2 (EC 4.1.1.50) (AdoMetDC
 2) (SamDC 2) [Contains: S-adenosylmethionine decarboxylase 2 alpha
 chain; S-adenosylmethionine decarboxylase 2 beta chain].
 GN Name=Amd2;
 OS Mus spratus (Western wild mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=99359841; PubMed=10430664;
 RA Persson K., Heby O., Berger P.G.;
 RT "The functional intronless S-adenosylmethionine decarboxylase gene (Idc)
 of the mouse (Amd-2) is linked to the ornithine decarboxylase gene (Odc)
 on Chromosome 12 and is present in distantly related species of the
 genus Mus.";
 RL J. Biol. Chem. 270:5642-5648 (1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Spine;
 RX MEDLINE=95137575; PubMed=7890685; DOI=10.1074/jbc.270.10.5642;
 RA Persson K., Holm I., Heby O.;
 RT "Cloning and sequencing of an intronless mouse S-adenosylmethionine
 decarboxylase gene coding for a functional enzyme strongly expressed
 in the liver.";
 RL J. Biol. Chem. 270:5642-5648 (1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ILE-70.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98285531; PubMed=9620866;
 RA Nishimura K., Liisanantti M., Muta Y., Kashiwagi K., Shirahata A.,
 RA Janne M., Kankare K., Janne O.A., Igarashi K.;
 RT "Structure and activity of mouse S-adenosylmethionine decarboxylase
 gene promoters and properties of the encoded proteins.";
 RL Biochem. J. 332:651-659 (1998).
 CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
 adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -I- COFACTOR: Pyruvoyl group.
 CC -I- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
 aminopropyl moiety required for spermidine and spermine
 biosynthesis from putrescine.
 CC -I- SUBUNIT: Heterotetramer of two alpha and two beta chains (By
 similarity).
 CC -I- TISSUE SPECIFICITY: Widely expressed. Particularly abundant in
 liver.
 CC -I- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
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 CC
 CC EMBL; Z23077; CAA80614.1; -;
 DR PIR; A55948; A55948.
 DR HSSP; P17707; I17B.
 DR MGD; MGI:133311; Amd2.
 DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IDA.
 DR InterPro; IPR001985; SAM_decarbox.
 DR Pfam; PF01536; SAM_decarbox; 1.
 DR ProDom; PD002379; SAM_decarbox; 1.

QY 28 FEPEKLELWFFPHKKSITTEKTLRNIGMDRWIEILKVKCEVLSMKTKELDAFLSE 87
 Db 11 FEGTEKLELWFSQODAS-KGSGDLRIPRFWDKLELVHCLISVTKDKQEAIVLSE 69
 QY 88 SSLFVDPDKLTKMTCTGTTTTLFCLEKLFQIVEQELSWAFETTOGGKYKPF-----KVFYSR 143
 Db 70 SSMFVSKRRFILKTCGTTLLQALVPLELARE-----YCGPDGIGNFFYSR 116
 QY 144 RCLFPCQAAIHONWADEVLYLNKFDNGKSYSGRNDKSNHNLVTVETDRSTPKGKE 203
 Db 117 KNFKPNHQBYPHNFHEVEFLNQIPFGAAVCMGRIN-SDCWLYTLTDIP-----DE 169
 QY 204 Y-IEDDDETEVLMTLDPCCASKFVCGPEASTTALVEPNEDKGNLGYOMTKNRLDEI 262
 Db 170 YVISQPDQTLLEILMSLDPVMDQF-----YMKEGVTANDVT 206
 QY 263 YVNSAQSDLSFHHDAPAFPCGYSNNMILAKEYYTLHVTPEKGSYASFEINIPV--F 320
 Db 207 RVSGIRDLITGVIDATMFPSPCGYSNMKSGDGTWTIHTIPDFSVFETNVSLLTY 266
 QY 321 DISQKQDNLDVLLHILNVQPRFESMTFTKKNYQNSFOKLLSINESLPDYIKLDKIVY 380
 Db 267 D-----DLISKVDVDFKPKFVTTLFW--QSSKCTTSCAQKIEGFRVRDQFA 315
 QY 381 DLDDYHLFYMKLQK 394
 Db 316 QFNDYNFVFTSFAK 329

RESULT 15

DCAM_BOVIN STANDARD; PRT; 334 AA.
 AC P50243;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
 DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
 GN Name=AMD1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hill J.R., Morris D.R.;
 RT "Regulation of translation of S-adenosylmethionine decarboxylase mRNA";
 RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 209-232 FROM N.A.
 RX MEDLINE=86304300; PubMed=3017942;
 RA Mach M., White M.W., Neubauer M., Degen J.L., Morris D.R.;
 RT "Isolation of a cDNA clone encoding S-adenosylmethionine decarboxylase. Expression of the gene in mitogen-activated lymphocytes";
 RL J. Biol. Chem. 261:11697-11703(1986).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -1- COFACTOR: Pyruvoyl group.
 CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
 CC -1- SUBUNIT: Heterotetramer of two alpha and two beta chains (By similarity).
 CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
 CC
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 CC
 CC
 DR EMBL; M95605; AAA30359.1; --
 DR EMBL; M14289; AAA30360.1; --
 DR PIR; I45851; I45851.
 DR HSSP; P17707; IJEN.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM decarbox; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
 FT CHAIN 1 67 S-adenosylmethionine decarboxylase beta chain.
 FT CHAIN 68 334 S-adenosylmethionine decarboxylase alpha chain.
 FT SITE 67 68 Cleavage (nonhydrolytic).
 FT MOD_RES 68 68 Pyruvic acid (Ser).
 FT ACT_SITE 8 8 Important for catalytic activity (By similarity).
 FT ACT_SITE 11 11 Important for catalytic activity (By similarity).
 FT ACT_SITE 82 82 Important for catalytic activity (By similarity).
 SQ SEQUENCE 334 AA; 38364 MW; D8AFB98C9DD8A1E9 CRC64;

Query Match 22.3%; Score 473; DB 1; Length 334;

Best Local Similarity 30.8%; Pred. No. 2e-28;

Matches 116; Conservative 69; Mismatches 138; Indels 56; Gaps 10;

QY 22 LDSTDAPEGPEKLELWFFPHKKSITT-EKTLRNIGMDRWIEILKVKCEVLSMKTKEL 80
 Db 1 MEAHFEGTEKLELWFFSRQDPDANQSGDLRTIPSEWDILLKDVQCSIIISVTKDKQ 60
 QY 81 DAPLSESLFVDFHDKLTKMTCTGTTTTLFCLEKLFQIVEQELSWAFETTOGGKYKPF--- 137
 Db 61 EAVLVSESSMFVSKRRFILKTCGTTLLKALVPLELKLARD-----YSGPDSI 107
 QY 138 -KVFYSRRCFLFPCKQAAIHONWADEVLYLNKFDNGKSYSGRNDKSNHNLVTVETDR 196
 Db 108 QSFYGRKFMKFSHQGYPHRNFOEIEFLNAPNGAAYCMGRMN-SDCWLYTLTDLDFPE 166
 QY 197 STPKGEYIEDDDTEFEVLMTLDPCCASKFVCGPEASTTALVEPNEDKGNLGYOMTKN 256
 Db 167 S-----RVINQPDQTLLEILMSLDPVMDQFYM-----KGVTAQDVRE 206
 QY 257 TRLDEIYVNSAQSDLSFHHDAPAFPCGYSNNMILAKEYYTLHVTPEKGSYASFEIN 316
 Db 207 SGIRDLIPGSVIDATM-----FNPCGYSNMKSGDGTWTIHTIPDFSVFETN 258
 QY 317 IPVFDISQKQDNLDVLLHILNVQPRFESMTFTKKNYQNSFOKLLSINESLPDYIKLD 376
 Db 259 -----LSQTSYD--DLIRKVVVEFKGFKFVTTLFWN--QSSKCTTSLSSPKIEGFKRLD 309
 QY 377 KIVYDLDYHLFYMKLQK 395
 Db 310 CQALFNDYNFVFTSFAK 328

Search completed: May 11, 2005, 22:52:28

Job time : 96.5567 secs

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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:42:53 ; Search time 21.3058 Seconds
(without alignments)

1806.392 Million cell updates/sec

Title: US-10-732-923-408

Perfect score: 2097

Sequence: 1 MAVLSAADASPVSAIGFEGY.....LLCWEEDADAMEEKAGVLDE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2097	100.0	400	2 T03947	adenosylmethionine
2	1682.5	80.2	393	2 S69191	adenosylmethionine
3	1657	79.0	398	2 T04099	adenosylmethionine
4	980	46.7	357	2 S68990	adenosylmethionine
5	971	46.3	361	2 T01934	adenosylmethionine
6	961.5	45.9	363	2 S49222	adenosylmethionine
7	954	45.5	377	2 T10708	adenosylmethionine
8	951.5	45.4	360	2 S52662	adenosylmethionine
9	946.5	45.1	353	2 T06515	probable adenosylm
10	944	45.0	381	2 T10707	adenosylmethionine
11	879	41.9	361	2 T12613	adenosylmethionine
12	874.5	41.7	369	2 T10750	probable adenosylm
13	869.5	41.5	362	2 T51378	adenosylmethionine
14	466	22.2	368	2 T22361	adenosylmethionine
15	423	20.2	334	1 DCHYDM	adenosylmethionine
16	420	20.0	334	1 DCHUDM	adenosylmethionine
17	420	20.0	334	2 A55948	adenosylmethionine
18	415	19.8	333	1 DCRTDM	adenosylmethionine
19	396	18.9	335	2 S72197	adenosylmethionine
20	372.5	17.8	396	1 DCBYDM	adenosylmethionine
21	108.5	5.2	530	2 S65773	glutamy1-trna redu
22	108.5	5.2	530	2 G86233	hypothetical prote
23	100	4.6	603	2 G82738	gamma-glutamyltran
24	96.5	4.6	410	2 AH3376	glycosyltransferas
25	96	4.6	593	2 S65470	pyruvate decarboxy
26	95.5	4.6	1307	2 T35944	probable beta-gala
27	94	4.5	1165	2 S11446	parasporal crystal
28	92	4.4	689	2 F81286	probable polysacch
29	91.5	4.4	560	2 B86661	hypothetical prote

RESULT 1

T03947

adenosylmethionine decarboxylase (EC 4.1.1.50) - maize

N;Alternate names: S-adenosylmethionine decarboxylase

C;Species: Zea mays (maize)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T03947

R;Michael, A.J.

submitted to the EMBL Data Library, September 1996

A;Reference number: Z15155

A;Accession: T03947

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-400 <MC>

A;Cross-references: UNIPROT:O24575; EMBL:Y07767; PIDN:CAA69075.1

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase

P;78/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match

Best Local Similarity 100.0%; Score 2097; DB 2; Length 400;

Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

oxoglutarate dehyd
nitrite reductase
LDL-receptor-relat
rf2 nuclear reator
glutamate synthase
alcohol dehydrogen
DNA helicase homol
hypothetical prote
hypothetical prote
hypothetical prote
nitrite reductase
N-acetylornithine
beta-N-acetylhexos
glycine cleavage s
polygalacturonase
hypothetical prote

ALIGNMENTS

30 90.5 4.3 967 2 F82668
31 90 4.3 336 2 JB0215
32 90 4.3 4753 1 A47437
33 89.5 4.3 549 2 T03983
34 89.5 4.3 1538 2 AF0432
35 89 4.2 352 2 G82719
36 89 4.2 453 2 G69494
37 89 4.2 1653 2 T14758
38 88.5 4.2 543 2 E96616
39 88.5 4.2 661 2 T46364
40 88 4.2 360 2 JG0170
41 88 4.2 390 2 G69044
42 88 4.2 883 2 E82102
43 88 4.2 983 2 AG2381
44 87.5 4.2 534 2 B97352
45 87 4.1 713 2 H64464

QY 1 MAVLSAADASPVSAIGFEGYKRLITTFSEAPVFDPHGRLRALGRAQIDSVLDLARCT 60
DB 1 MAVLSAADASPVSAIGFEGYKRLITTFSEAPVFDPHGRLRALGRAQIDSVLDLARCT 60
QY 61 IVSELSNKDFDSYLVSESSLFYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKY 120
DB 61 IVSELSNKDFDSYLVSESSLFYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKY 120
QY 121 SRGTFFPGAQAPAPHRSPFSEVAALNRYFGGLKSGGNAYVIGDPAPGQKWHFYATEYP 180
DB 121 SRGTFFPGAQAPAPHRSPFSEVAALNRYFGGLKSGGNAYVIGDPAPGQKWHFYATEYP 180
QY 181 EQPMVNLWCMTGLDKKACVFKTNADGNTTCAKEMTKLSGISEIIPENEICDFDFEPC 240
DB 181 EQPMVNLWCMTGLDKKACVFKTNADGNTTCAKEMTKLSGISEIIPENEICDFDFEPC 240
QY 241 GYSMNAIHGSAFSTIHVTPEDEGFSYASYEVMGLDATALSYGDLVKRVLRCFGPSEFSVAV 300
DB 241 GYSMNAIHGSAFSTIHVTPEDEGFSYASYEVMGLDATALSYGDLVKRVLRCFGPSEFSVAV 300
QY 301 TIFGGRGHAGTWGKALGAEVYDCNNVVEQELPGGGLLVYQSFCAAEADAVATSPKSPVHCF 360
DB 301 TIFGGRGHAGTWGKALGAEVYDCNNVVEQELPGGGLLVYQSFCAAEADAVATSPKSPVHCF 360
QY 361 DGENVESAPPPMKDKYKLANLLCWESEADAMEEKAGVLDE 400
DB 361 DGENVESAPPPMKDKYKLANLLCWESEADAMEEKAGVLDE 400

RESULT 2

S69191
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - wild barley
C;Species: Hordeum chilense (wild barley)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69191
R;Dresselhaus, T.; Barcelo, P.; Hagel, C.; Loerz, H.; Humbeck, K.
Plant Mol. Biol. 30, 1021-1033, 1996
A;Title: Isolation and characterization of a Tritordeum cDNA encoding S-adenosylmethionine decarboxylase
A;Reference number: S69191; MUID:96270379; PMID:8639739
A;Accession: S69191
A;Molecule type: mRNA
A;Residues: 1-393 <DRE>
A;Cross-references: UNIPROT:Q42829; EMBL:X83881; NID:g1403043; PIDN:CAA58762.1; PID:g1403043
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; eukaryotic type
F;1-71/Product: adenosylmethionine decarboxylase beta chain #status predicted <MAT1>
F;72-393/Product: adenosylmethionine decarboxylase alpha chain #status predicted <MAT2>
F;247-262/Region: PEST sequence
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match	80.2%;	Score 1682.5;	DB 2;	Length 393;	
Best Local Similarity	82.7%;	Pred. No. 6.6e-135;			
Matches	324;	Conservative 25;	Mismatches 38;	Indels 5;	Gaps 3;

QY	9	ASPVSAIGFEGYKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSLSNK	68
DB	2	AAPVSAIGFEGYKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSLSNK	61
QY	69	DFDSYVLSSESLPIYPLKIVIKTCGTTKLLTTPRILELAELSPLAAVKYSGRTFIPP	128
DB	62	DFDSYVLSSESLPIYKQKIVIKTCGTTKLLTTPRILELAELSPLAAVKYSGRTFIPP	121
QY	129	GAQPAPHRFSSEVAALNRYFGGLKSGGNAYVIGDPAPGQKWHVFYATEYPPQMVNLE	188
DB	122	GAQPAPHRFSSEVDVNLRYFGHLNNGGNAYVIGDPAPGQKWHVIYATEYPPQMVNLE	181
QY	189	MCMTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISSEIIPMEICDFDFPEPCYSMAIH	248
DB	182	MCMTGLDKTKASVFFKTHADGHVSCAKEMTKLSGISDIIPMEICDFDFPEPCYSMAIN	241
QY	249	GSASFTHVTPEDGFSYASVEVMGLDATALSYGDLVKRLVRCFGPSEFSVAVTIFGGRGH	308
DB	242	GSASFTHVTPEDGFSYASVEVMGLDATALSYGDLVKRLVRCFGPSEFSVAVTIFGGRGH	301
QY	309	AGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADV--ATSPKSVFHCDFGENYE	366
DB	302	AATWKKLDAEAYDCNNMVEQELPGGGLLVYQSFCAAEADV--ENVE	359
QY	367	SAPPPMKDYKLANLLCWEEADAMEEKAGVL	398
DB	360	SG-HPLVKEGKLANLLAWRAEESLEEGTGA	390

RESULT 3

T04099
adenosylmethionine decarboxylase homolog [similarity] - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Mar-2004
C;Accession: T04099
R;Michael, A.J.
submitted to the EMBL Data Library, September 1996
A;Description: Spermidine biosynthesis in rice.
A;Reference number: Z15210
A;Accession: T04099
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-398 <MIC>
A;Cross-references: EMBL:Y07766; PIDN:CAA69074.1
A;Experimental source: cv. Nipponbare
A;Note: this sequence appears to lack the residues necessary to form an active site
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

Query Match	79.0%;	Score 1657;	DB 2;	Length 398;	
Best Local Similarity	80.8%;	Pred. No. 9.8e-133;			
Matches	325;	Conservative 23;	Mismatches 48;	Indels 6;	Gaps 4;

QY	1	MAVLSAADASPVSAIGFEGYKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLARCT	60
DB	1	MGDLAADPPVSAIGFEGYKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLARCT	60
QY	61	IVSELNKKDFDSYVLSSESLPIYPLKIVIKTCGTTKLLTTPRILELAELSPLAAVKY	120
DB	61	IVSELNKKDFDSYVLSSESLPIYPLKIVIKTCGTTKLLTTPRILELAELSPLAAVKY	120
QY	121	SGTFTFPGQAPHRFSSEVAALNRYFGGLKSGGNAYVIGDPAPGQKWHVFYATEYPP	180
DB	121	SRGMFIFPSAQAPAPLRFSSEVAALNRYFGHLKSGGNAYVIGDPAPGQKWHVIYATQHP	180
QY	181	EOPMVALEMCMTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISSEIIPMEICDFDFPEPC	240
DB	181	EOPMVTLEMCMTGLDKKKACVFFKTSADGHTSCAKEMTKLSGISDIIPMEICDFDFPEPC	240
QY	241	GYSMNAIHGSAFSTHVTPEDEGFSYASVEVMGLDATALSYGDLVKRLVRCFGPSEFSVAV	300
DB	241	GYSMNAIHGSAFSTHVTPEDEGFSYASVEVMGLDATALSYGDLVKRLVRCFGPSEFSVAV	300
QY	301	TIFGGRGHAGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADV--AVATSPKSVFH	358
DB	301	TIFGGRGHAGTWAKELNADAYKCNMVEQELPGGGLLVYQSFCAAEADV--AVATSPKSVFH	360
QY	359	CFDGENVESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE	400
DB	361	CFAENMNVN-PAVKEG-KLGNLLPWGE--DALEENDGVFDE	398

RESULT 4

S68990
adenosylmethionine decarboxylase (EC 4.1.1.50) - Madagascar periwinkle
N;Alternate names: S-adenosyl-L-methionine decarboxylase proenzyme
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S68990
R;Schroeder, G.; Schroeder, J.
Eur. J. Biochem. 228, 74-78, 1995
A;Title: cDNAs for S-adenosyl-L-methionine decarboxylase from Catharanthus roseus, heterologous
in the active enzyme, and a conserved region in the 5' mRNA leader.
A;Reference number: S68989; MUID:95188916; PMID:7883014
A;Accession: S68990
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-357 <SCH>
A;Cross-references: UNIPROT:Q42679; EMBL:U12573; NID:g758693; PID:g758695
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match	46.7%;	Score 980;	DB 2;	Length 357;	
Best Local Similarity	51.6%;	Pred. No. 2.4e-75;			
Matches	204;	Conservative 56;	Mismatches 87;	Indels 48;	Gaps 8;

QY	9	ASPVSAIGFEGYKRLKLEITFSEAPVFDPHGRGLRALSRQAIDSVDLRLARCTIVSLSNK	68
DB	2	ALPASAIIGFEGYKRLKLEISFFESSFFADPDGKGLRALNKSQIDEILEPAECTIVDSLSNQ	61
QY	69	DFDSYVLSSESLPIYPLKIVIKTCGTTKLLTTPRILELAELSPLAAVKYSGRTFIPP	128
DB	62	YLDYSYVLSSESLFVYYPYKIIKTCGTTKLLTTPAILKLAESLSLVRRNRYKTRGSPFP	121
QY	129	GAQPAPHRFSSEVAALNRYFGGLKSGGNAYVIGDPAPGQKWHVFYATEYPPQ	185
DB	122	GAQSFHRFSSEVELLDNRYFGKLGESNAFIMGNDQDP--QKWHVYSASVGSQSDDTY	180
QY	186	NLEMCMTGDKKKACVFFKTNADGNTTCAKEMTKLSGISSEIIPMEICDFDFPEPCYSMN	245
DB	181	TLEMCMTGDKREKASVFKS---ESSAALMTTRGIRKILPDSSEICDFDFPEPCYSMN	236

A;Description: A spinach cDNA with homology to S-adenosylmethionine decarboxylase.

A;Reference number: S49222

A;Accession: S49222

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-363 <BOL>

A;Cross-references: UNIPROT:P46255; EMBL:X81414; NID:g547471; PID:g547472

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase

F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.9%; Score 961.5; DB 2; Length 363;
Best Local Similarity 51.5%; Pred.No.9.2e-74;
Matches 204; Conservative 49; Mismatches 92; Indels 51; Gaps 10;

QY 12 VSAIGFEGEYKRLIEITFSBPVFDVDPHGRLRALSPAQIDSVDLDLARCTIVSLSLNKDFD 71
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 ISAIGFEGFEKRLIEITFPSIFVDPEGKLRAQLDEILGPAECTIVDSLANSVD 62

QY 72 SYVLSSSLFIYPLKVITCGTTKLLLTPIRILELAELSMPAAVKYSRGTFIFPGAQ 131
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 SYVLSSSLFIYAYKIIIKTCGTTKLLRAPPTLRLAGKSLDVKSVRVTRGSFIFPGAQ 122

QY 132 PAPHRSFSEVALNRYFGGLXSGGNAYVGDPARPGQKHVFYATETP---EQPMVNLE 188
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 SYAHSFSEVAVLGDGYFKLAGSAFAFVNGDDPAKP-QRWHVYSAGAETISFEEPVTTL 181

QY 189 MCMTGLDKKKACVFFFTKNADGNTTCAKEWTKLSGISIIPEMBEICDFDEPCGYSMAIH 248
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 182 MCMTGLKKKASVFFKSQSPN----AAVMTESSGIRKILPDSCIKCDFDEPCGYSMAIE 237

QY 249 GSASFTHITPEDGFYSAYEVNGLDATALSYGDLVKRVLCFSPSEFSVANVTFGGRGH 308
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 238 GPAISTHITPEDGFYSAFVAGYGLKKTLNLQNLVERVLACFEPSEFSIAI-----H 290

QY 309 AGTWGKALGAENV-DQNNVVEQELPGGL-----LVYQSFCAAEDAVATSPKSVFH 358
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 291 AETAANSMBHNCVNVNGYSREE--GGTEELGFGAASVYQKFCKASTGFGATNK---- 343

QY 359 CFPDENVESAPPMMKKDYKANLLCWEEBADAMEEK 394
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 344 -----PRPALX-----CCWKE--DKFEEE 360

RESULT 7
T10708
adenosylmethionine decarboxylase (EC 4.1.1.50) 2 - clove pink
N;Alternate names: S-adenosylmethionine decarboxylase 2
C;Species: Dianthus caryophyllus (Clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10708
R;Lee, M.M.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, October 1995
A;Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase
A;Reference number: Z17089
A;Accession: T10708
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-377 <LEE>
A;Cross-references: UNIPROT:Q39677; EMBL:U38527; NID:gl155241; PID:gl155242
A;Experimental source: cv. White Sim; carnation petal
C;Function:
A;Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (S-deoxy-S-ac
A;Pathway: polyamine biosynthesis
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;84/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.5%; Score 954; DB 2; Length 377;
Best Local Similarity 52.7%; Pred.No.4.2e-73;
Matches 205; Conservative 47; Mismatches 87; Indels 50; Gaps 11;

QY 12 VSAIGFEGEYKRLIEITFSBPVFDVDPHGRLRALSPAQIDSVDLDLARCTIVSLSLNKDFD 71

Db 18 ISAIGFEGEKRLIEISFFEPGIFVDPGEGRLRALSKAHLDEILGPACTIVDSLANESVD 77
Qy 72 SYVLSSSLFIYPLKVIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTFIFPGAQ 131
Db 78 SYVLSSSLFVYSYKIIKTCGTTKLLNSIPILRLAETLFLDVKSVRVTRGSFIFPGAQ 137
Qy 132 PAPHRFSERVEALNRYFGLKSGGNAYVIGDPAFCQKWHVYATEYP--EOPMVNLEM 199
Db 138 SPHRFSERVEAVLDNYFAKLGAGSKAIVMGSPGKPK--QKWHVYSATAETNYDDFVYLEM 196
Qy 190 CMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAIHG 249
Db 197 CMTGLDKERKASVFEKS-----QSASAAVMTSESSGIRKILPDSVICDFDFEPCGYSMAIIEG 252
Qy 250 SAFSTIHTVPEDGFSYASVEVMGLDATALSYDGLVLRVLCRFGPSEFSVAVTIFGGRGHA 309
Db 253 PAVSTIHTVPEDGFSYASVEAVGVLDVLDNLVERVLACPEPKGFSIAV-----HA 305
Qy 310 --GTWKGALCAEYVDCN--NMVE-----QELPGGGLLVYQSCFAEDAVATSPKSVFH 358
Db 306 DTDADTKVLAR---NCSVNVIYSGREEGIEELGLGSGVYQKFC-----GTAP----- 352
Qy 359 CPGENVESAPPMKKDYKLANLLCWEE 387
Db 353 -----VCPAPAKTKL-----CCWKEE 369

RESULT 8
S52662
adenosylmethionine decarboxylase (EC 4.1.1.50) TUB13 [similarity] - potato
C;Species: Solanum tuberosum (potato)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52662; S28047
R;Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.; Burch, L.R.; Davies, H.V.; Sta
plant Mol. Biol. 26, 327-338, 1994
A;Title: Characterization of the S-adenosylmethionine decarboxylase (SAMDC) gene of pota
A;Reference number: S52662; MUID:95036004; PMID:7948879
A;Accession: S52662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <ARI>
A;Cross-references: UNIPROT:Q04694; GB:S74514; NID:9807093; PIDN:AAB32507.1; PID:9807094
R;Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie, L.A.; Pearce, S.R.; Flav
Plant Mol. Biol. 20, 641-651, 1992
A;Title: Expression and sequence analysis of cDNAs induced during the early stages of tu
A;Reference number: S28046; MUID:93081725; PMID:1450379
A;Accession: S28047
A;Molecule type: mRNA
A;Residues: 1-173, 'S', 175-256, 'T', 258-290, 'V', 292-304, 'I', 306-360 <TAY>
A;Cross-references: EMBL:Z11680; GB:S51455; NID:G21484; PIDN:CAA77742.1; PID:G21485
C;Genetics:
A;Gene: TUB13
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;73/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.4%; Score 951.5; DB 2; Length 360;
Best Local Similarity 51.4%; Pred. No. 6.5e-73;
Matches 203; Conservative 47; Mismatches 94; Indels 51; Gaps 8;

Qy 11 PVSAIGFEGEKRLIEITFSAPVFDPHGRLRALSPAQIDSVLDLACTIVSELSNKNDF 70
Db 6 PVSAIGFEGEKRLIEISFVEPLFADPNKGRSLSKAQLDEILGPAECTIVDNLNDYV 65
Qy 71 DSVLSSSLFIYPLKVIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTFIFPGA 130
Db 66 DSVLSSSLFVYSYKIIKTCGTTKLLAIPILRLAETLSLKVDVTRGSFIFPGA 125
Qy 131 QPAPHRFSERVEALNRYFGLKSGGNAYVIGDPAFCQKWHVYATEYPEQ---PMVNL 187
Db 126 QSPHRRHFSERVEAVLDGFKLAAGSKAVIMGSPDKT-QKWHVYSASAGPVQNDPVYTL 194

Qy 188 EMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAI 247
Db 185 EMCMTGLDKERKASVFEK-----EESAAHWTVSGIRKILPKSEICDFEPEPCGYSMAI 240
Qy 248 HGSASFSTIHTVPEDGFSYASVEVMGLDATALSYDGLVLRVLCRFGPSEFSVAVTIFGGRG 307
Db 241 EGAAVSTIHTVPEDGFSYASVESGVNPKTMELGVLVERVLACFEPAEFSIAL----- 293
Qy 308 HAGTWKAL-----CAEYVDCNMMVEQELPGGGLLVYQSCFAEDAVATSPKSVFHCFD 361
Db 294 HADVATKLLERTCSDVDPKGYSLAESPEFEGGSIYQKFC---TRTPYCSPPKSVLKG-- 349
Qy 362 GENVESAPPMKKDYKLANLLCWEEADAMEEKAG 396
Db 350 -----CWKE-----EKEG 358

RESULT 9
T06515
probable adenosylmethionine decarboxylase (EC 4.1.1.50) - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06515
R;Carrasco, P.; Marco, F.
submitted to the EMBL Data Library, June 1996
A;Description: Pea S-adenosylmethionine decarboxylase.
A;Reference number: Z15729
A;Accession: T06515
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-353 <CAR>
A;Cross-references: UNIPROT:Q43820; EMBL:U60592; NID:g1421750; PIDN:AAB03865.1; PID:g142
A;Experimental source: cv. Alaska
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.1%; Score 946.5; DB 2; Length 353;
Best Local Similarity 53.9%; Pred. No. 1.7e-72;
Matches 193; Conservative 56; Mismatches 98; Indels 11; Gaps 5;

Qy 12 VSAIGFEGEKRLIEITFSAPVFDPHGRLRALSPAQIDSVLDLACTIVSELSNKNDF 71
Db 3 VSAIGFEGEKRLIEISFSPGLFSDPQGRGLRSLTKSQLDEILAPAECTIVSSLANEDVD 62
Qy 72 SYVLSSSLFIYPLKVIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTFIFPGAQ 131
Db 63 SYVLSSSLFVYAYKLIKTCGTTKLLSIPILKLADSLNVRSVRYTRGSFIFPGAQ 122
Qy 132 PAPHRFSERVEALNRYFGLKSGGNAYVIGDPAFCQKWHVYATE---YEPQMVNLE 188
Db 123 SPHRRHFSERVEAVLDGFFGKLGSGSMAYILGG--SDEAQNWHIYCASSDSVSPEGSVVYLE 181
Qy 189 MCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAI 248
Db 182 MCMTGLDKERKASVFEK-----QTGSAEMTVNSGIRKILNSEICDFDFEPCGYSMAI 237
Qy 249 GSASFSTIHTVPEDGFSYASVEVMGLDATALSYDGLVLRVLCRFGPSEFSVAVTIFGGRGH 308
Db 238 GSAVSTIHTVPEDGFSYASVETAGYDLKAINLNMVNRVLACFQPTFEFSVAHV--DNASK 296
Qy 309 AGTWKALCAEYVDCNMMVEQELPGGGLLVYQSCFAEDAVATSPKSVFHCFDGENVE 366
Db 297 SFEQGLLDVKGCCBEKSHQGLMGSGSVVYQKFC---LKTSYCGSPRSTLKCWKDEDEE 352

RESULT 10
T10707
adenosylmethionine decarboxylase (EC 4.1.1.50) 1 - clove pink
N;Alternate names: S-adenosylmethionine decarboxylase 1
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10707; T10787

R;Lee, M.M.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, October 1995
A;Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase
A;Reference number: Z17089
A;Accession: T10707
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-381 <LEE>
A;Cross-references: UNIPROT:Q39676; EMBL:U38526; NID:g1155239; PID:g1155240
A;Experimental source: cv. White Sim; carnation petal
R;Kim, Y.J.; Lee, M.M.; Chang, K.S.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z17144
A;Accession: T10787
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-381 <KIM>
A;Cross-references: EMBL:U94786; NID:g2406584; PID:g2406585
A;Experimental source: strain White sim
C;Genetics:
A;Gene: gscd39
C;Function:
A;Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (S)-deoxy-5-adenosyl-L-methionine
C;Pathway: polyamine biosynthesis
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;93/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 45.08; Score 944; DB 2; Length 381;
Best Local Similarity 55.54; Pred. No. 3e-72;
Matches 197; Conservative 48; Mismatches 84; Indels 26; Gaps 7;

QY 12 VSAIGFEGYKRLIETPSEAPVFDPHGRGLRALSRQAIDSVLDLARCTIVSELSNKKDFD 71
DB 27 LSAIGFEGYKRLIETPSEAPVFDPHGRGLRALSRQAIDSVLDLARCTIVSELSNKKDFD 86

QY 72 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPLAAVKYSGRTFFPGAQ 131
DB 87 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPLAAVKYSGRTFFPGAQ 146

QY 132 PAHRFSEEEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP--EQPMVNLEM 189
DB 147 SYHRFSEEEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP--EQPMVNLEM 205

QY 190 CMTGLDKKACVFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMAIHG 249
DB 206 CMTGLDKKASVFFKS-----ESSAAVMTETSGIRKILPDSALCDFDFEPCGYSMAIEG 261

QY 250 SAFSTHTVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFGPSEFSVAVTIFGGRGHA 309
DB 262 PAVSTHTITPDEGFSYASFEAVGYDLKIVDQNLVERVLNCFQPREFSIAVS----- 314

QY 310 GTWKGKALGAEVYDCNNV-----BQELPGGLLVYQSF--CAEADAVATSPK 354
DB 315 DTADKVL--BOYCAVNVAGYCBREGGVEGLGVGSLYKFGKVTATYVGLNKSPPK 367

RESULT 11
T12613
adenosylmethionine decarboxylase (EC 4.1.1.50) - common sunflower
N;Alternate names: S-adenosylmethionine decarboxylase
C;Species: Helianthus annuus (common sunflower)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
R;Eliasson, A.; Hammann, P.; Steinmetz, A.
submitted to the EMBL Data Library, May 1998
A;Description: Coding sequence for an S-adenosylmethionine decarboxylase from sunflower
A;Reference number: Z17552
A;Accession: T12613
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-361 <ELI>
A;Cross-references: UNIPROT:O65354; EMBL:AF066078; NID:g3153905; PID:g3153906

A;Experimental source: cultivar HA300; mature pollen
C;Genetics:
A;Gene: SAD
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 41.94; Score 879; DB 2; Length 361;
Best Local Similarity 53.84; Pred. No. 9.2e-67;
Matches 199; Conservative 47; Mismatches 96; Indels 28; Gaps 11;

QY 13 SAIGFEGYKRLIETPSEAPVFDPHGRGLRALSRQAIDSVLDLARCTIVSELSNKKDFD 72
DB 3 SAIGFEGYKRLIETPSEAPVFDPHGRGLRALSRQAIDSVLDLARCTIVSELSNKKDFD 62

QY 73 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPLAAVKYSGRTFFPGAQ 132
DB 63 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPLAAVKYSGRTFFPGAQ 122

QY 133 AHRFSEEEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP-----PMVN 186
DB 123 FHRFSEEEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP-----PMVN 181

QY 187 LEMCMTGLDKKACVFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFEPCGYSMA 246
DB 182 LEMCMTGLSKRNASVFFKS-----ESSAAVMTETSGIRKILPDSALCDFDFEPCGYSMA 237

QY 247 IHGSAFSTHTVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFGPSEFSVAVTIFGGR 306
DB 238 IEGDALSTHTVTPEDGFSYASFEAVGYDLKIVDQNLVERVLNCFQPREFSVA 292

QY 307 GHAGTWKGKALGAEVYDCN-----NMVE---OELPG--GGLLVYQSFCAEADAVATSPKSVFH 358
DB 293 GNEVV-VKOLLENNDVNVKGVNVEETKFEVLGGGSMVYGF-ARGGSCGSPRSTLH 350

QY 359 -CF-DGNEVE 366
DB 351 RCWSETENEE 360

RESULT 12
T10750
probable adenosylmethionine decarboxylase (EC 4.1.1.50) - leaf mustard
C;Species: Brassica juncea (leaf mustard)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
R;Lee, T.; Liu, J.J.; Pua, E.C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17116
A;Accession: T10750
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-369 <LEE>
A;Cross-references: UNIPROT:O49972; EMBL:U80916; NID:g2662405; PID:g2662406
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 41.74; Score 874.5; DB 2; Length 369;
Best Local Similarity 50.54; Pred. No. 2.3e-66;
Matches 187; Conservative 51; Mismatches 89; Indels 43; Gaps 10;

QY 12 VSAIGFEGYKRLIETPSEAPVFDPHGRGLRALSRQAIDSVLDLARCTIVSELSNKKDFD 71
DB 3 VSAIGFEGYKRLIETPSEAPVFDPHGRGLRALSRQAIDSVLDLARCTIVSELSNKKDFD 62

QY 72 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPLAAVKYSGRTFFPGAQ 131
DB 63 SYLVSESLFIYPLKIVIKTCGTTKLLTTPRIELAEELSMPLAAVKYSGRTFFPGAQ 122

QY 132 PAHRFSEEEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP-----EQP 183
DB 123 PFHRFSEEEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP-----EQP 180

Search completed: May 11, 2005, 22:59:08
Job time : 23.3058 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:40:28 ; Search time 81.6495 Seconds
(without alignments)
1620.151 Million cell updates/sec

Title: US-10-732-923-406

Perfect score: 2118

Sequence: 1 MTVTIKELTNHNYIDHELSEA.....KIVYDLDDVHLYFMKLQKXI 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 segs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2118	100.0	396	15	US-10-310-154-456 Sequence 456, App
2	2118	100.0	396	15	US-10-369-493-22338 Sequence 22338, A
3	709.5	33.5	478	15	US-10-436-327-3 Sequence 3, Appli
4	681	32.2	503	15	US-10-369-493-3386 Sequence 3386, Ap
5	565	26.7	369	15	US-10-369-493-2553 Sequence 2553, Ap
6	471	22.2	348	9	US-09-925-300-1167 Sequence 1167, Ap
7	470	22.2	334	15	US-10-341-434-12 Sequence 12, Appl
8	470	22.2	334	15	US-10-341-434-20 Sequence 20, Appl
9	470	22.2	334	15	US-10-341-434-127 Sequence 127, App
10	470	22.2	334	17	US-10-753-267-50 Sequence 50, Appl
11	434	20.5	368	15	US-10-369-493-5286 Sequence 5286, Ap
12	434	20.5	368	15	US-10-369-493-5297 Sequence 5297, Ap
13	390	18.4	398	16	US-10-767-701-46359 Sequence 46359, A

14	388	18.3	416	15	US-10-425-114-57997 Sequence 57997, A
15	388	18.3	416	15	US-10-425-114-67343 Sequence 67343, A
16	386	18.2	397	16	US-10-767-701-47033 Sequence 47033, A
17	385	18.2	422	15	US-10-425-114-36776 Sequence 36776, A
18	377	17.8	355	15	US-10-424-599-249854 Sequence 249854, A
19	377	17.8	355	15	US-10-424-599-249859 Sequence 249859, A
20	377	17.8	356	15	US-10-425-114-46255 Sequence 46255, A
21	377	17.8	356	15	US-10-425-114-46648 Sequence 46648, App
22	372.5	17.6	400	15	US-10-310-154-458 Sequence 458, App
23	370	17.5	395	16	US-10-767-701-46141 Sequence 46141, A
24	368	17.4	355	15	US-10-424-599-249855 Sequence 249855, A
25	368	17.4	360	15	US-10-425-114-43048 Sequence 43048, A
26	368	17.4	360	15	US-10-425-114-46323 Sequence 46323, A
27	368	17.4	360	15	US-10-425-114-47297 Sequence 47297, A
28	368	17.4	450	16	US-10-437-963-147033 Sequence 147033, A
29	368	17.4	466	16	US-10-437-963-147475 Sequence 147475, A
30	365	17.2	363	14	US-10-380-913-4 Sequence 4, Appli
31	359.5	17.0	554	16	US-10-437-963-142921 Sequence 142921, A
32	358	16.9	395	16	US-10-437-963-142922 Sequence 142922, A
33	345	16.3	392	16	US-10-437-963-128930 Sequence 128930, A
34	343	16.2	331	15	US-10-425-114-71868 Sequence 71868, A
35	325.5	15.4	361	15	US-10-424-599-205003 Sequence 205003, A
36	306.5	14.5	359	16	US-10-437-963-166485 Sequence 166485, A
37	294	13.9	366	15	US-10-310-154-457 Sequence 457, App
38	266.5	12.6	224	15	US-10-424-599-205002 Sequence 205002, A
39	226	10.7	289	15	US-10-425-114-56960 Sequence 56960, A
40	224.5	10.6	305	15	US-10-425-114-39365 Sequence 39365, A
41	212	10.0	276	15	US-10-425-114-69727 Sequence 69727, A
42	172	8.1	216	15	US-10-425-114-45581 Sequence 45581, A
43	161	7.6	201	15	US-10-424-599-159442 Sequence 159442, A
44	136	6.4	203	15	US-10-425-114-56490 Sequence 56490, A
45	131.5	6.2	187	15	US-10-425-114-57416 Sequence 57416, A

ALIGNMENTS

RESULT 1

US-10-310-154-456
; Sequence 456, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luetby, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.

```

; APPLICANT: Miller, Philip W
; APPLICANT: Padmavathi, Manchikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Tennessee, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhaunguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 456
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-310-154-456

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Query Match      100.0%; Score 2118; DB 15; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.9e-186;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTVTIKELTNHNYIDHLSATLSDTAFAEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60
Db 1 MTVTIKELTNHNYIDHLSATLSDTAFAEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60

Qy 61 IEILKLVKCEVLSMKTKELDAPLLSSSLFVFDHKLTMKTCGTTTTLFCLKLFQIVEQ 120
Db 61 IEILKLVKCEVLSMKTKELDAPLLSSSLFVFDHKLTMKTCGTTTTLFCLKLFQIVEQ 120

Qy 121 ELSWAFRTTGGKYKPKFVYSRRCFLPCKQAAIHQNWADVDVYLNKFFDNGKSYSGVR 180
Db 121 ELSWAFRTTGGKYKPKFVYSRRCFLPCKQAAIHQNWADVDVYLNKFFDNGKSYSGVR 180

Qy 181 NDKSNHNLVYVTDRTSTPKGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240
Db 181 NDKSNHNLVYVTDRTSTPKGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240

Qy 241 PNEDKGHNLYGQMTKNTLDEIYVNSAQSDLSLPHHDAFAFTPCGYSSNMLAEKYYTTL 300
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Qy 301 HVTPEKWSVASPESNIPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQSFQ 360
Db 301 HVTPEKWSVASPESNIPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQSFQ 360

Qy 361 KLLSINESLPDYIKLKIYVDLDYHLYFYMKLQKKI 396
Db 361 KLLSINESLPDYIKLKIYVDLDYHLYFYMKLQKKI 396

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RESULT 2
US-10-369-493-22338
; Sequence 22338, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B

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; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22338
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22338

Query Match      100.0%; Score 2118; DB 15; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.9e-186;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTVTIKELTNHNYIDHLSATLSDTAFAEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60
Db 1 MTVTIKELTNHNYIDHLSATLSDTAFAEGPEKLEIWFPPHKKSIITTEKTLRNIGMDRW 60

Qy 61 IEILKLVKCEVLSMKTKELDAPLLSSSLFVFDHKLTMKTCGTTTTLFCLKLFQIVEQ 120
Db 61 IEILKLVKCEVLSMKTKELDAPLLSSSLFVFDHKLTMKTCGTTTTLFCLKLFQIVEQ 120

Qy 121 ELSWAFRTTGGKYKPKFVYSRRCFLPCKQAAIHQNWADVDVYLNKFFDNGKSYSGVR 180
Db 121 ELSWAFRTTGGKYKPKFVYSRRCFLPCKQAAIHQNWADVDVYLNKFFDNGKSYSGVR 180

Qy 181 NDKSNHNLVYVTDRTSTPKGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240
Db 181 NDKSNHNLVYVTDRTSTPKGKEYIEDDDTFFVLMTELDPCEASKFVCGPEASTTALVE 240

Qy 241 PNEDKGHNLYGQMTKNTLDEIYVNSAQSDLSLPHHDAFAFTPCGYSSNMLAEKYYTTL 300
Db 241 PNEDKGHNLYGQMTKNTLDEIYVNSAQSDLSLPHHDAFAFTPCGYSSNMLAEKYYTTL 300

Qy 301 HVTPEKWSVASPESNIPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQSFQ 360
Db 301 HVTPEKWSVASPESNIPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQSFQ 360

Qy 361 KLLSINESLPDYIKLKIYVDLDYHLYFYMKLQKKI 396
Db 361 KLLSINESLPDYIKLKIYVDLDYHLYFYMKLQKKI 396

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RESULT 3
US-10-436-327-3
; Sequence 3, Application US/10436327
; Publication No. US20030224970A1
; GENERAL INFORMATION:
; APPLICANT: Mahanty, Sanjoy K
; APPLICANT: Heiniger, Ryan W
; APPLICANT: Skalchunes, Amy R
; APPLICANT: Pan, Huaqin
; APPLICANT: Tarpey, Rex
; APPLICANT: Shuster, Jeffrey R
; APPLICANT: Tanzer, Matthew M
; APPLICANT: Hamer, Liebeth
; APPLICANT: Adachi, Kiichi
; APPLICANT: DeZwaan, Todd M
; APPLICANT: Lo, Sze Chung C
; APPLICANT: Montenegro-Chamorro, Maria V
; APPLICANT: Frank, Sheryl A
; APPLICANT: Darveau, Blaise A
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF INHIBITORS OF
; TITLE OF INVENTION: S-ADENOSYLMETHIONINE DECARBOXYLASE AS ANTIBIOTICS
; FILE REFERENCE: 2151US
; CURRENT APPLICATION NUMBER: US/10/436,327
; CURRENT FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 478
; TYPE: PRT

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; ORGANISM: Magnaporthe grisea
US-10-436-327-3

Query Match      33.5%; Score 709.5; DB 15; Length 478;
Best Local Similarity 35.2%; Pred. No. 2.3e-56;
Matches 162; Conservative 86; Mismatches 115; Indels 97; Gaps 15;

QY 14 IDHLSATLDSTDAFEGPEKLLIWFPPHKKSI---TTEKTLRNIGMDRWIEILKLVKCE 70
DB 23 INHDVAQDLDSGAFEGPEKLLIWFAPSPALPLGTKEGLKSPVSDNNVEMLDIVNCK 82
QY 71 VLSMKTKELDALFLSSSLFVFDHKLTKMTCTGTTTTLFCLEKLPQI----- 117
DB 83 ILSVVOSSVVVDAYLLSSSMFVFPKILKTCGTTTLLGLAQLRIAAVDAGFPVHNAS 142
QY 118 -VQELSWAPRTTQGGKVPKVFYSRRCLFPCKQAAIHONWADEVYDYLNKFDPGKSY 176
DB 143 SVDEKAAA-----TPRVFYSRKNFLFDRQGRPHRSKWQVKYLDSPFEGGSAY 193
QY 177 SVGRNDSKNHNLVYVTE-----TDRSTPKGKEYI-----EDDDTEFVLMTL 219
DB 194 MVGKMN-GDHWLYVMTSPGSTALTTPQTPPAGELMRIPTGLQTAASREDDTEFLVMTDL 252
QY 220 DPCASKFVCGPASTTA-----LVEPNEDKGNLGY 251
DB 253 DPNKQFYL-EQASALACKQATLAQQAREEAHAALDKAASTDEQLVSEALTTEGHALGT 311
QY 252 QMTKNTLRDLIYVNSA-QSDSLSFHDDAFAPTCPGYSNNIL-----AEKYYIT 299
DB 312 VSDTCGLSDVYPKSKYDPDARI---DAYMFEPCGSANGVVPAPPDATGAQGGNEHYFT 367
QY 300 LHYTPKGSYASFPESNIPVFDISQKQDNLVLLHLNVPQREFSMTFT-KTYQNQS 358
DB 368 VHYTPENCYSASFETNVPG---GQNGRETADIIHGVGIFKPGFSVTLFEGKGRGEN 424
QY 359 FQKL---LSINESLPYIKDKIVYDLDYHLYFMKLOKK 395
DB 425 GTRADQRLRV-DNVPGVYQLDKIVHEDDYDLVFRFYQRE 463

RESULT 4
US-10-369-493-3386
; Sequence 3386, Application US/10369493.
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3386
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3386

Query Match      32.2%; Score 681; DB 15; Length 503;
Best Local Similarity 32.5%; Pred. No. 1.1e-53;
Matches 161; Conservative 85; Mismatches 128; Indels 122; Gaps 13;

QY 2 TVTIKELTNYIDHLSATLDSTDAFEGPEKLLIWFPPHKKSI---TTEKTLRNIGMD 58
DB 14 TFSPEGTPTLTINHVAALDSTNAFEGPEKLLIWFAPSAKALPAGVKEGLKAVNPD 73
QY 59 RWIEILKLVKCEVLSMKTKELDALFLSSSLFVFDHKLTKMTCTGTTTTLFCLEKLPQIV 118

; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2553

Query Match      26.7%; Score 565; DB 15; Length 369;
Best Local Similarity 36.1%; Pred. No. 3.2e-43;
Matches 139; Conservative 75; Mismatches 135; Indels 36; Gaps 13;

QY 14 IDHLSATLDSTDAFEGPEKLLIWF-FPHKKSIIT-EKT---LRNIGMDRWIEILKLVK 68
DB 7 VDOENSEEF-NTSSFEGPEKLLIWFSAPIKTNLSAGERKANLGLKAVSRNDWDMLAAQ 65
QY 69 CEVLSMKTKELDALFLSSSLFVFDHKLTKMTCTGTTTTLFCLEKLPQIVQEQLSWAFRT 128
DB 66 CKVLSVYVNSEIDAYLLSSSMFVFAHKKILKTCGTTTLLASLPRLLEI-----A 115
QY 129 TQGGKVPKVFYSRRCLFPCKQAAIHONWADEVYDYLNKFDPGKSYSGVRNDKSNHN 188
DB 116 SSVGFDRPURIIFYSRKNFLYPERQLAPHTSWEVEYQLQFPFSGGCVVVGPTNK-NHWH 174
QY 189 LYVTETDRSTPKGKEYIEDDDTEFVLMTLDPDECASKF-----VCGPEASTTALVEP 241
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Db 175 LFSLDADYSLL-EDSLDPEDETLEVLMTDMSPEISQFYAPSLDVRSGDDYVREKN 233
Qy 242 NEDKGNLGYOMTKVTRLDRIYVNSAQDSLSFHDAFAFTPCGYSSNMILAEKYVYTLH 301
Db 234 NLSGCHILGSVADESGVRDLCSSTDKAVL---DAFQPEPIGFSNNMIYKDR-YATIH 288
Qy 302 VTPKKGHSYASFENIPVFDISQKQNDLVLLHILNVFQPREFMTFTTKYQNSQFQK 361
Db 289 VTPQHCYSYASFETNVSQFQGRSISETIE---KTVKTFGANKFCLTLFOAKGASQ--EK 343
Qy 362 LLSIN-ESLPDYIKLDKIVVDLDY 385
Db 344 HFSAKLSFSYSKREEIFVDFFGY 368

RESULT 6

US-09-925-300-1167
; Sequence 1167, Application US/099255300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 1167
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1167

Query Match 22.2%, Score 471; DB 9; Length 348;

Best Local Similarity 30.3%; Pred. No. 1.3e-34;

Matches 115; Conservative 70; Mismatches 138; Indels 56; Gaps 10;

Qy 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRNIGMDRWIEILKLVKCEVLSMKTKEL 80
Db 15 MEAAHFEFEGTEKLELVWFVSRQPDANQSGDLRTIPRSEWDILKQVCCSIISVTKDKQ 74
Qy 81 DAFLLSESSLFVFDHKLTMKTCGTTTLFCLEKLFQIVEQELSFAFRTTQGGYKPF--- 137
Db 75 EAYVLSSESMFVSKRFRILKTCGTTLLKALVPLLLKARD-----YSGFDSI 121
Qy 138 -KVFSYRCFLFPCKQAAIHONWADEVYLNKFPDNGKYSVGRNDKSNHNLVYVTTDR 196
Db 122 QSPFYSRKNFMKPSHQGYPHRFQEEIEFLNAIFPNGAAYCMGRMN-SDCWLYLTLDPE 180
Qy 197 STPKGEYIEDDDTFFVLMTELDPECAKSFVCPPEASTTALVEPNEDKGNLYQMTKN 256
Db 181 S-----RVISQPDQTLSEILMSLDPVMDQFYM-----KOGVTAKOVIRE 220
Qy 257 TRLDEIVVNSAQDSLSFHDAFAFTPCGYSSNMILAEKYVYTLHVTPEKGSYASPEFN 316
Db 221 SGIRDLPGSVIATM-----FNPCCGYSMGKSDGYTHITPEPEFSVSVETN 272
Qy 317 IPVFDISQKQNDLVLLHILNVFQPREFMTFTTKYQNSQFQKLSINESLPDYIKLD 376
Db 273 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKCRTVLASPKIEGPKRLD 323
Qy 377 KIVYDLDYHLFYMKLOKK 395
Db 324 CQSAFNDYNFVFTSFARK 342

RESULT 7

US-10-341-434-12

; Sequence 12, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-12

Query Match 22.2%, Score 470; DB 15; Length 334;

Best Local Similarity 30.3%; Pred. No. 1.5e-34;

Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

Qy 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRNIGMDRWIEILKLVKCEVLSMKTKEL 80
Db 1 MEAAHFEFEGTEKLELVWFVSRQPDANQSGDLRTIPRSEWDILKQVCCSIISVTKDKQ 60
Qy 81 DAFLLSESSLFVFDHKLTMKTCGTTTLFCLEKLFQIVEQELSFAFRTTQGGYKPF--- 137
Db 61 EAYVLSSESMFVSKRFRILKTCGTTLLKALVPLLLKARD-----YSGFDSI 107
Qy 138 -KVFSYRCFLFPCKQAAIHONWADEVYLNKFPDNGKYSVGRNDKSNHNLVYVTTDR 196
Db 108 QSPFYSRKNFMKPSHQGYPHRFQEEIEFLNAIFPNGAGYCMGRMN-SDCWLYLTLDPE 166
Qy 197 STPKGEYIEDDDTFFVLMTELDPECAKSFVCPPEASTTALVEPNEDKGNLYQMTKN 256
Db 167 S-----RVISQPDQTLSEILMSLDPVMDQFYM-----KOGVTAKOVIRE 206
Qy 257 TRLDEIVVNSAQDSLSFHDAFAFTPCGYSSNMILAEKYVYTLHVTPEKGSYASPEFN 316
Db 207 SGIRDLPGSVIATM-----FNPCCGYSMGKSDGYTHITPEPEFSVSVETN 258
Qy 317 IPVFDISQKQNDLVLLHILNVFQPREFMTFTTKYQNSQFQKLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKCRTVLASPKIEGPKRLD 309
Qy 377 KIVYDLDYHLFYMKLOKK 395
Db 310 CQSAFNDYNFVFTSFARK 328

RESULT 8

US-10-341-434-20
; Sequence 20, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:

; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 334
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-341-434-20

Query Match      22.2%; Score 470; DB 15; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.5e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLELWFFPHKSIIT-EKTLRNIGMDRWIEILKLVKCEVLNKKTKEL 80
DB 1 MEAAHFEGETEKLEWVFSRQPDANQSGDLRTIPRSEWDILLKDVQCSIIISVTKDKQ 60
QY 81 DAFLLSESSLFVDPDHKLTKMTCTGTTTLFCLEKLFQIVQEQLSWAFRTTGGKYKFP--- 137
DB 61 EAYVLSSESMFVSKRRFILKTCGTGTTLLKALVPLLLKARD-----YSGFDSI 107

QY 138 -KVFYSRRCLFPCKQAAIHONWADEVYLNKFPDNGKSYSGVRNDSKNHNLVYVTTETDR 196
DB 108 QSFYYSRKNFMKSHQYPRNFQEEIEFLNAPNGAGYCMGRMN-SDCWLYLTLDLDFPE 166

QY 197 STPKGKEYIBDDDETEVLMTLDPBCASKFVCGPEASTTALVEPNEDKGHNILGYQMTKN 256
DB 167 S-----RVISQPDOTLEILMSELDPVMDQFYM-----KGVTAQDVTR 206

QY 257 TRLDEIYVNSAQSDLSFHHDFAFPTCGYSSNMILAKEYYTLHTVTPKGNYSASPESN 316
DB 207 SGIRDLIPGVIDATM-----FNPCGYSMNGKSDGTYYTHITHTPEPEFSYVSFETN 258

QY 317 IPVFDISQKQDNLDVLLHILNVQPREFSMTFTTKNYQNSQPKLLSINESLPDYIKLD 376
DB 259 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKCRTVLASPKIEGFKRLD 309

QY 377 KIVYDLDVHLYFMKLOKK 395
DB 310 QCSAMENDYNFVTSFAKK 328

RESULT 10
US-10-753-267-50
; Sequence 50, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodrigue-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13866, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MPI03-003PARNOMIN
; CURRENT APPLICATION NUMBER: US/10753,267
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-50

Query Match      22.2%; Score 470; DB 17; Length 334;

; ORGANISM: Homo sapiens
US-10-341-434-20

Query Match      22.2%; Score 470; DB 15; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.5e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLELWFFPHKSIIT-EKTLRNIGMDRWIEILKLVKCEVLNKKTKEL 80
DB 1 MEAAHFEGETEKLEWVFSRQPDANQSGDLRTIPRSEWDILLKDVQCSIIISVTKDKQ 60
QY 81 DAFLLSESSLFVDPDHKLTKMTCTGTTTLFCLEKLFQIVQEQLSWAFRTTGGKYKFP--- 137
DB 61 EAYVLSSESMFVSKRRFILKTCGTGTTLLKALVPLLLKARD-----YSGFDSI 107

QY 138 -KVFYSRRCLFPCKQAAIHONWADEVYLNKFPDNGKSYSGVRNDSKNHNLVYVTTETDR 196
DB 108 QSFYYSRKNFMKSHQYPRNFQEEIEFLNAPNGAGYCMGRMN-SDCWLYLTLDLDFPE 166

QY 197 STPKGKEYIBDDDETEVLMTLDPBCASKFVCGPEASTTALVEPNEDKGHNILGYQMTKN 256
DB 167 S-----RVISQPDOTLEILMSELDPVMDQFYM-----KGVTAQDVTR 206

QY 257 TRLDEIYVNSAQSDLSFHHDFAFPTCGYSSNMILAKEYYTLHTVTPKGNYSASPESN 316
DB 207 SGIRDLIPGVIDATM-----FNPCGYSMNGKSDGTYYTHITHTPEPEFSYVSFETN 258

QY 317 IPVFDISQKQDNLDVLLHILNVQPREFSMTFTTKNYQNSQPKLLSINESLPDYIKLD 376
DB 259 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKCRTVLASPKIEGFKRLD 309

QY 377 KIVYDLDVHLYFMKLOKK 395
DB 310 QCSAMENDYNFVTSFAKK 328

RESULT 9
US-10-341-434-127
; Sequence 127, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-341-434-127

Query Match      22.2%; Score 470; DB 15; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.5e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLELWFFPHKSIIT-EKTLRNIGMDRWIEILKLVKCEVLNKKTKEL 80
DB 1 MEAAHFEGETEKLEWVFSRQPDANQSGDLRTIPRSEWDILLKDVQCSIIISVTKDKQ 60
QY 81 DAFLLSESSLFVDPDHKLTKMTCTGTTTLFCLEKLFQIVQEQLSWAFRTTGGKYKFP--- 137
DB 61 EAYVLSSESMFVSKRRFILKTCGTGTTLLKALVPLLLKARD-----YSGFDSI 107

QY 138 -KVFYSRRCLFPCKQAAIHONWADEVYLNKFPDNGKSYSGVRNDSKNHNLVYVTTETDR 196
DB 108 QSFYYSRKNFMKSHQYPRNFQEEIEFLNAPNGAGYCMGRMN-SDCWLYLTLDLDFPE 166
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Best Local Similarity 30.3%; Pred. No. 1.5e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10

QY 22 LDSTDAFEGPEKLEIWFPHKKSIIT--EKLRLNIGMDRWIEILKLKVEVLSMKKTKEL 80
Db 1 MEAAHFEGTEKLEVWFSPROQDPANQSGDGLRTIPSEWDILLKDVQCSIISVTKTDKQ 60

QY 81 DAFLLSSSSLFVDFHKLMTKTCGTTTTLFCLEKLFQIVEQLSWAFRTTQGGKYKPF--- 137
Db 61 EAYVLSSSMFVSKRRFILTKTCGTTTLLKALVPLKLARD-----YSGFDSI 107

QY 138 -KVPYSRCFLFPCQAAIHQWNADEVLYLNKFPDNGSKYSVGRNDKSNHNLYYTETDR 196
Db 108 QSFYSKRNFKMPSHQGYPHENFOBEIEFLNAIPNGAGYCWGRMN-SDCVLYLTLDPE 166

QY 197 STPKGEYIEDDSTFEVLMTLELPECASKVKVCGPEASTTALVEBNEKGHNLYQYMTKN 256
Db 167 S-----RVISQDDQLBELMSLELPAVMDQPYM-----KQVTAQDVTR 206

QY 257 TRLDEIVYNSAQSDLSLGFHDAFATPCGYSSNMILAEYYTTLHVTPEKWSVASPESN 316
Db 207 SGIRDLLPGSVIDATM-----FNPCGYSMWGMSDGTWTHTITEPEFSYVSFTN 258

QY 317 IPVEDISQGDNDLVLLHILNVQPRFESMTFFTKNYQNSQFQKLLSINSLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKRTVLASPKIEGFKELD 309

QY 377 KIVYDLDYHLFYMKLQKK 395
Db 310 QQSAMFNDYNFVFTSFACK 328

RESULT 11
US-10-369-493-5296
; Sequence 5296, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
; OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5296
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5296

Query Match 20.5%; Score 434; DB 15; Length 368;
Best Local Similarity 30.9%; Pred. No. 3.7e-31;
Matches 125; Conservative 72; Mismatches 129; Indels 78; Gaps 16

QY 9 TNNHYIDHELSATLSDTDAFEGPEKLEIWFPHKKSIITTEKLRNIGMDRWIEILKLK 68
Db 7 TNFAVQTHPVKAP-DEEYFFEGAEKLELWFCSSQTNET--RSRLIIPREIDAMLDIAR 63

QY 69 CEVLSMKKTKELDAPFLSSESLFVDFDHKLTKWTCTGTTTTLFCLEKLFQIVBQELSWAFRT 128
Db 64 CKILSHKHNESIDSYVLSSESLFISDNRVILKTCGTTRLAALPVIMQ-----LAGAY-- 116

QY 129 TQGGKYKPFKYVYRRRCFLFPCQAAIHQWNADEVLYLNKFPDNGSKYSVGRNDKSNHN 188
Db 117 --AGLDQVQSYYYSRKNFLPDPQLPSLHKNFDAEVEYLDSPFVDGHAYCLG-SLKQDRWY 173

QY 189 LYVETDRSTPKGEYIEDDSTFEVLMTLELPECASKVCGPEASTTALVEBNEKGHN 248

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;
; BENCHMARK: 146
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone.ID: LIB4767-001-F3_FLI.pep
US-10-425-114-67343

Query Match      18.3%   Score 388; DB 15; Length 416;
Best Local Similarity 33.1%; Pred. NO. 7.5e-27;
Matches 111; Conservative 56; Mismatches 110; Indels 58; Gaps 14;

QY    24  STDAFSGPEKLLIEMFPFHKKSIITTE---KTLRNIGMDRWIEILKLVKCEVLMSMKTKEL 80
Db    36  SVTGFGEFKLEISF--SEAPVADPSGEGRLASRAQIDSVLDLARCTIVELSNDNF 93

QY    81  DAPLLESSELFVEDHKLWKMTCGTTTTLFCLEKLFQIVQEELSMAFRFTGGKYKPF-KV 139
Db    94  DSYLVSESSLFVYPYKIVIKTCGTTKLLAIPAILEABELL-----LPLAAV 141

QY    140 FYSSRCFLPCKQAALHQNWADVLYNKFF----DNGSKSYSGRNDK-SNHKNLYVTET 194
Db    142 KYSRGTFTIPPAQSPSHKNFADEVAFNLRFPGGLKGSGNAYVIIGDSAKPGQKHVVY--- 198
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Qy 195 DRSTPKGKEYIEDDETEFEVLMTLDEPCASKFVCGPEASTTALVEPNEDKGHNL-GYOM 253
Db 199 -----AAEHPEEPVVTLEMCMTGLDKKASVFF-----KTTA-----DGYSLCAKEM 240
Qy 254 TKNTRLDEIYVNSAQSDLSFHHDFAFTPCGYSSNMILAKEYYYTLHVTPEKGSYASF 313
Db 241 TKLSGISDI-IPEMEICD-----PDFEPCGYSMNAVHGPA-LSTIHVTPEDGFSYASY 291
Qy 314 ESNIPVFDISQKQDNLDVLJLHILNVFPREFSMT 348
Db 292 E-----VMGFNPGSFSYGDLVKRVLCRCFGPTEFSVT 322
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Search completed: May 11, 2005, 22:57:56
Job time : 83.6495 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:39:42 ; Search time 26.1959 Seconds
(without alignments)
1128.461 Million cell updates/sec

Title: US-10-732-923-406
Perfect score: 2118
Sequence: 1 MTVTIKELTNHNYIDHELSEA.....KIVYDLDYHLFMYKLQKKI 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	785	37.1	424	4	US-09-248-796A-18169
2	471	22.2	348	4	US-09-949-016-10038
3	470	22.2	334	4	US-09-917-254-54
4	112	5.3	753	4	US-09-248-796A-19291
5	108.5	5.1	585	4	US-09-107-532A-5494
6	107.5	5.1	749	4	US-09-562-737-95
7	107	5.1	336	1	US-07-667-276A-8
8	99	4.7	1661	2	US-08-882-083-2
9	99	4.7	1661	3	US-08-558-107-2
10	99	4.7	1661	3	US-09-243-539-2
11	99	4.7	2184	4	US-09-417-485D-6
12	96.5	4.6	822	4	US-08-851-567B-28
13	96.5	4.6	822	4	US-09-248-796A-19917
14	96.5	4.6	1189	4	US-08-851-567B-26
15	95	4.5	944	2	US-08-867-941-23
16	95	4.5	944	3	US-09-074-658-23
17	94.5	4.5	554	3	US-09-319-989-6
18	94.5	4.5	2777	4	US-09-543-681A-6124
19	94	4.4	485	2	US-08-724-394A-8
20	94	4.4	695	3	US-09-134-001C-4341
21	94	4.4	754	4	US-09-710-279-1296
22	93.5	4.4	1183	2	US-08-447-031A-2
23	93	4.4	3418	3	US-08-755-587-44
24	92.5	4.4	2325	4	US-08-697-826A-10
25	92.5	4.4	2938	5	PCT-US94-00198-3
26	92	4.3	414	4	US-09-107-433-3170
27	92	4.3	423	4	US-09-583-110-3518

28	92	4.3	484	6	5171673-8	Patent No. 5171673
29	92	4.3	484	6	5171673-8	Patent No. 5171673
30	92	4.3	487	6	5171673-6	Patent No. 5171673
31	92	4.3	487	6	5171673-6	Patent No. 5171673
32	92	4.3	610	4	US-09-248-796A-17036	Sequence 17036, A
33	92	4.3	749	2	US-08-568-459A-6	Sequence 6, Appli
34	92	4.3	749	2	US-08-487-826B-6	Sequence 6, Appli
35	92	4.3	749	3	US-09-210-288-6	Sequence 6, Appli
36	92	4.3	2304	3	US-09-324-867-4	Sequence 8, Appli
37	92	4.3	2319	1	US-08-212-133A-8	Sequence 6, Appli
38	92	4.3	2319	1	US-08-474-503-6	Sequence 6, Appli
39	92	4.3	2319	2	US-08-670-707A-6	Sequence 6, Appli
40	92	4.3	2319	3	US-09-037-601-6	Sequence 6, Appli
41	92	4.3	2319	3	US-09-315-179-6	Sequence 6, Appli
42	92	4.3	2319	4	US-09-523-656-28	Sequence 28, Appli
43	92	4.3	2319	5	PCT-US94-13200-6	Sequence 6, Appli
44	91	4.3	686	4	US-09-107-532A-5118	Sequence 5118, Ap
45	90.5	4.3	592	3	US-08-845-258-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1

US-09-248-796A-18169
; Sequence 18169, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18169
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18169

Query Match	37.1%;	Score 785;	DB 4;	Length 424;
Best Local Similarity	43.8%;	Pred. No. 1e-71;		
Matches	176;	Conservative 64;	Mismatches 114;	Indels 50; Gaps 12;
Qy	13	YIDHLSATLSDTADEGEPEKLEIWFPPHKKSIITTEKTLRNICMDRWIELKLVKCEVL	72	
Db	50	YSNHLSATLSDTADEGEPEKLEIWFPPHKKSIITTEKTLRNICMDRWIELKLVKCEVL	107	
Qy	73	SMKKTELDAFLSSESLFVDFHKLTMKTCGTTTTLFCLEKLFQIVEQEL--SWAFRTQ	130	
Db	108	SKVSSNLDAFLSSESLFVDFHKLTMKTCGTTTTLFCLEKLFQIVEQEL--SWAFRTQ	167	
Qy	131	GGKYKPKFYSPRCFLPCKQAAIHQWADVDYLNKPFDKGKSYSGVGNKSNHNL	190	
Db	168	QSK-NIYQIFYSRRSFMFDRQIHVHGNWQEEVKLLNQYFNNKSYIVGN--TNHLY	223	
Qy	191	V-----TETDRSTPKGKEYIDDETFEVLMTDELDPKASKFVCGPEASTAL	238	
Db	224	VGGNGTKPKPVAFTTTTTP-----VVDCTLEIMTQLSLEASQFVTRKPGDTA	276	
Qy	239	VEPNEDKGNHLYQMTKNTLRDLFIYNSAQ-----DSDLSPHHDFAFTPCGYSSNMI	291	
Db	277	IDSNDHLDLGGQELKQTLGNELFKPKQPTMPGLSSSPIKIHDFGFAFTPCGFSNSI	336	
Qy	292	LAEKYYTTHVTPEKGSVASPESNIPVDFISQKQDNLDVLHILNVFQPREFTMTFT	351	
Db	337	-NESNYTTHVTPEPGWSVASFETNM-----IGDYKAIVDKCINVPFGQFMVTFLT	387	

Qy 352 KNYNQSFQKLLSINESLPDYIKLDKIVYDLDVYHLFYMKLQKK 395
Db 388 -NTDMKFECLD-----DYKNHRELDVEDYKLYFVIRQ 434

RESULT 2

US-09-949-016-10038
; Sequence 10038, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10038
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10038

Query Match 22.2%; Score 471; DB 4; Length 348;
Best Local Similarity 30.3%; Pred. No. 1.2e-39;
Matches 115; Conservative 70; Mismatches 138; Indels 56; Gaps 10;

Qy 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRNICMDRWIEILKVKCVLSMKTKEL 80
Db 15 MEAAHFFEGTEKLELVWFSRQPDANQSGDLRTIPRSEWDILLKDVQCSIISVTKTDQ 74

Qy 81 DAFLLSESLFVFDHKLTMTKTCGTTTLFCLEKLFQIVEQELSFAFTTQGGKYKPF--- 137
Db 75 EAYVLSSESMFVSKRRPILKTCGTTLLKALVPLLLKARD-----YSGFDSI 121

Qy 138 -KVFYSRRCLFPCKQAAIHQNAWEDVDYLNKFFDNGKSYSGVRNDKSNHNLVYVTETDR 196
Db 122 QSFYSRKNFMKPSHQYPRNFQEELEFLNAIFPNAGAYCMGRMN-SDCWLYLTLDPE 180

Qy 197 STPKGKEYIEDDDTEFVLMTELDPECASKFVCGPEASTTALVEPNEDKGHNLYQMTKN 256
Db 181 S-----RVISQPDQTLLEILSELDPVMDQFYM-----KDGVTAKDVTRE 220

Qy 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYYTLHTVTPKGMWSYASFSN 316
Db 221 SGIRDLIPGSVIDATM-----FNPCGYSMNGKSDGTWYTHITPEPEFSVSPETN 272

Qy 317 IPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQKLLSINESLPDYIKLD 376
Db 273 -----LSQTSYD--DLIRKVVVEFKPKFTVTLFVN--QSSKCRTVLASPKIEGFKRLD 323

Qy 377 KIVYDLDVYHLFYMKLQKK 395
Db 324 QCSAMFNDYNFVFTSFAKK 342

RESULT 3

US-09-917-254-54
; Sequence 54, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254

; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-54

Query Match 22.2%; Score 470; DB 4; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.4e-39;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

Qy 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRNICMDRWIEILKVKCVLSMKTKEL 80
Db 1 MEAAHFFEGTEKLELVWFSRQPDANQSGDLRTIPRSEWDILLKDVQCSIISVTKTDQ 60

Qy 81 DAFLLSESLFVFDHKLTMTKTCGTTTLFCLEKLFQIVEQELSFAFTTQGGKYKPF--- 137
Db 61 EAYVLSSESMFVSKRRPILKTCGTTLLKALVPLLLKARD-----YSGFDSI 107

Qy 138 -KVFYSRRCLFPCKQAAIHQNAWEDVDYLNKFFDNGKSYSGVRNDKSNHNLVYVTETDR 196
Db 108 QSFYSRKNFMKPSHQYPRNFQEELEFLNAIFPNAGAYCMGRMN-SDCWLYLTLDPE 166

Qy 197 STPKGKEYIEDDDTEFVLMTELDPECASKFVCGPEASTTALVEPNEDKGHNLYQMTKN 256
Db 167 S-----RVISQPDQTLLEILSELDPVMDQFYM-----KDGVTAKDVTRE 206

Qy 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYYTLHTVTPKGMWSYASFSN 316
Db 207 SGIRDLIPGSVIDATM-----FNPCGYSMNGKSDGTWYTHITPEPEFSVSPETN 258

Qy 317 IPVFDISQKQDNLDVLLHILNVFPQREFSMTFTTKYQNSQKLLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVVVEFKPKFTVTLFVN--QSSKCRTVLASPKIEGFKRLD 309

Qy 377 KIVYDLDVYHLFYMKLQKK 395
Db 310 QCSAMFNDYNFVFTSFAKK 328

RESULT 4

US-09-248-796A-19291
; Sequence 19291, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19291
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19291

Query Match 5.3%; Score 112; DB 4; Length 753;
Best Local Similarity 20.8%; Pred. No. 0.026;
Matches 94; Conservative 63; Mismatches 131; Indels 164; Gaps 24;

Qy 4 TIKELTNHNYIDHE-----LSATLDSDTDAFEGPEKLEIWM 38
Db 131 TLKDM--RNYLDRQKYSNDNLVEFYLSILPGSELGLDGLGTAIEPTDV--TVKKLLDP- 185

QY 39 FPHKKSITTEKLRN-----ICMDRWIBILKLVKCEVLSMKTKKELDAPLSSSLFV 92
Db 186 -----KTSQTEKTWNRVSKRVKFRVITTDQAKLDNIAMSVEYDGDILLEYEMFLNV 240
QY 93 FD-----HKTMKTGTTTTLFCLEKLFQIVBOELSWAFRTTGGKKPKPKVPSRRCFL 147
Db 241 CDDEELRHRYE-----EKLKFP-----KYELKV-----C-- 265
QY 148 FPCQQAIAHONWADVDYLNKFPDNGKSYSGVRNDSNHNLYVTETDRSTPKGKEVIED 207
Db 266 -PKQ-AHQDIKNQMB--DMILINKSLFC-----WNLFPDWCDAKT-----IND 307
QY 208 DDET-----FEVLMTELDPPCASKFVCG-----PEASTALV 239
Db 308 LDENKVISYLOIFONEGLGILFAYVMSDISPSKEKIVKLSAYDINKRKPDSQ---L 364
QY 240 EPNEDEKGNLYGOMTKNRLDEIVVNS-----ADDSLSFHDAPAFPTPCGYSSNMILAEK 295
Db 365 NPEDDKDAELLELEADATLEDETSSQYLLPQDEVILGLEYSKT-----KNSVLASR 419
QY 296 YY--YTLHVTPEKWSVASPESNIPV-----FDISQCKODNLDVLLHILNVFOP 342
Db 420 IIVNYIHL---REYNLASCKRDGKTKLADIORTGIDUTNTKEDFLCSLAIIVYTYEA 476
QY 343 REFSMTFTTKNYQNSQFQKLLSINESLPDIK 374
Db 477 -----PKNY-NRAIQLEVKILESNDPNVK 499

RESULT 5
US-09-107-532A-5494
; Sequence 5494, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5494:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES

ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...585
SEQUENCE DESCRIPTION: SEQ ID NO: 5494:
US-09-107-532A-5494

Query Match 5.1%; Score 108.5; DB 4; Length 585;
Best Local Similarity 21.6%; Pred. No. 0.04;
Matches 103; Conservative 66; Mismatches 174; Indels 133; Gaps 22;

QY 8 LTNHYIDHEL SATLSDTA FEGPEKLEIWFPHKKSIT-TEKT-----LNIGM 57
Db 2 LTFEYKEETQMETSINIPIYVDKEXLLE-----KPVTKKKTVDRCCLDNREVTR 54
QY 58 DRWIEILKLVKCEVLSMKTKKELDAPLSSSLFVFDHKLTMK-TGTTTTLFCLEKLFQ 116
Db 55 DEFVEILNQSQFIPSKTRKNGNDKESFVETRVIIILDVNTVKDEKGVVDLSKDSRYL 114
QY 117 IVEQELS-----WAPRTTQGGKY-----KPFK-VFYSRRCLFPCKQAAIHQ-----N 158
Db 115 STEKVLISINLVHNSAFAIOKSIRYSENLYKIVFLKKAITDYGMVAEYVYLKKNIPG 174
QY 159 WADEVLYLNKFDNG-KSYSGVRNDSNHNLYVTETDRSTPKGKEYIEDDDTFFVLMT 217
Db 175 CDDNVNASNRMPFGYKSDAVIINEDNMLDITELPIDFTMTCKNCQSDSGREYE-LVN 233
QY 218 ELDPCEKAFVCGPEASTTALVEPNEDKGNLYGOMTKNRLD-----EIV----- 263
Db 234 ETD-----FV-----KLK-NDDKEEM--KQWFKDCLFDSSDMSEIYERLLTID 276
QY 264 ----VNSAODSLSFHHD---AFAFTP-----CGYSSNMILAEKYVYTLHVTPEKG 307
Db 277 MNLKLSKKNLCLFHNINPSASIFTSKTHSIFYC-HSSNCDISENFVGVWLILKKD 335
QY 308 WSYASF-----ESNIPVFDISQCKODNL-----DVL 334
Db 336 SRVETENMLENLDLVPTHFRKLKESKVLFDLTLESMDKLPRTIRNLEEMRRVVDLL 395
QY 335 HILNVFQPREFSMT-----FFTKNYQNSQFQKLLSINESLPDIKLD 376
Db 396 SDVNPFDSDSKSVTCILSGEQLAKKMSYYGKTYDIDCKNKLKSLMTFLIGLKLKD 451

RESULT 6
US-09-562-737-95
; Sequence 95, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-95

Query Match 5.1%; Score 107.5; DB 4; Length 749;
Best Local Similarity 21.4%; Pred. No. 0.075;
Matches 43; Conservative 36; Mismatches 73; Indels 49; Gaps 7;

QY 10 NNNYIDHEL SATLSDTA FEG---PEKLE-----IWFPFHKKSITTEKLRNIGMRWI 61
Db 10 NNNYIDHEL SATLSDTA FEG---PEKLE-----IWFPFHKKSITTEKLRNIGMRWI 61

Db 705 GLWILGCHNSDFRNRGWTALLKVSSCIPEGEEDDDYLDLEKIFSEDDDY 753

RESULT 9

US-08-558-107-2
; Sequence 2, Application US/08558107
; Patent No. 5910481
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,107
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-558-107-2

Query Match 4.7%; Score 99; DB 2; Length 1661;
Best Local Similarity 20.1%; Pred. No. 2;
Matches 70; Conservative 44; Mismatches 107; Indels 128; Gaps 16;
QY 131 GGYKPKFVFYSRRCLFPCKQAAIHQN-----WADEVYLNKFFDNGKSYSGVRNDK 183
DB 439 GRKYKVR-FMAYTDEFTKTRAIQHESGILGPLLYGEVDTLLIF-----KNQA 488
QY 184 SNHNLV---VTET---DRSTPKGEYIEDDDTEFVLMTEL-----D 220
DB 489 SRPNYIYPHGITDVRPLYSRRLPKGVKHLKD---FPILPGEIFKYKWTVTVEDGPTKSD 544
QY 221 PECA-----SKFVCGPEASTALVPE-----NEDKGNLGYQMTKNTLDELYVNSAQSDDL 272
DB 545 PRLTRYYSFVNNERDLASGLIGPLLCYKESVDQGNQIMSDKR--NVILSFVDENR 602
QY 273 SFH-----HDAFAFTPCGYSNNMILAEKYYTTLHTVPEKWSYASFESNIPVFDISQKQD 328
DB 603 SWYLTENIQRLPNPAGVQLE-----DPEFOASNMHSINGVYVDSLQ---- 645
QY 329 NLDVLLH-----ILNVQPRFSMTPTT----- 351
DB 646 -LSVCLHEVAYWYILSIGAQTDLFSVFFSGYTFKHKMVEDTLTLFPFSGETVFMSEN 704
QY 352 -----KNYQNSFOKLLSINESLP-----DYIKLDKIYVDLDDY 385
DB 705 GLWILGCHNSDFRNRGWTALLKVSSCIPEGEEDDDYLDLEKIFSEDDDY 753

RESULT 11

RESULT 10
US-09-243-539-2
; Sequence 2, Application US/09243539
; Patent No. 6130203
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/243,539
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/558,107
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-243-539-2

Query Match 4.7%; Score 99; DB 3; Length 1661;
Best Local Similarity 20.1%; Pred. No. 2;
Matches 70; Conservative 44; Mismatches 107; Indels 128; Gaps 16;
QY 131 GGYKPKFVFYSRRCLFPCKQAAIHQN-----WADEVYLNKFFDNGKSYSGVRNDK 183
DB 439 GRKYKVR-FMAYTDEFTKTRAIQHESGILGPLLYGEVDTLLIF-----KNQA 488
QY 184 SNHNLV---VTET---DRSTPKGEYIEDDDTEFVLMTEL-----D 220
DB 489 SRPNYIYPHGITDVRPLYSRRLPKGVKHLKD---FPILPGEIFKYKWTVTVEDGPTKSD 544
QY 221 PECA-----SKFVCGPEASTALVPE-----NEDKGNLGYQMTKNTLDELYVNSAQSDDL 272
DB 545 PRLTRYYSFVNNERDLASGLIGPLLCYKESVDQGNQIMSDKR--NVILSFVDENR 602
QY 273 SFH-----HDAFAFTPCGYSNNMILAEKYYTTLHTVPEKWSYASFESNIPVFDISQKQD 328
DB 603 SWYLTENIQRLPNPAGVQLE-----DPEFOASNMHSINGVYVDSLQ---- 645
QY 329 NLDVLLH-----ILNVQPRFSMTPTT----- 351
DB 646 -LSVCLHEVAYWYILSIGAQTDLFSVFFSGYTFKHKMVEDTLTLFPFSGETVFMSEN 704
QY 352 -----KNYQNSFOKLLSINESLP-----DYIKLDKIYVDLDDY 385
DB 705 GLWILGCHNSDFRNRGWTALLKVSSCIPEGEEDDDYLDLEKIFSEDDDY 753

SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-851-567B-26

Query Match 4.6%; Score 96.5; DB 4; Length 1189;
Best Local Similarity 20.4%; Pred. No. 2.1; Indels 133; Gaps 20;
Matches 88; Conservative 59; Mismatches 151;
Qy 7 ELTNHNYIDHLSATLSDTDAFEGPEKLLIWI-FFPHKKSIITTEKTLRNIGMDRWIE-IL 64
Db 68 QLFHRAIEGVGDTLADSAKPYADEQFLYNWDSFNHRYSTWAGKERLKFYAGYIDPTL 127
Qy 65 KLVKCEV-----LSMKYK-----ELDAFLSSESLFVFDHKLTMKTCGTTTLFCL 111
Db 128 RLNKTEIFTAFEGISQGLKSELVESKLDYLIISYDTLATDY-ITACQCKDKNTIFFI 186
Qy 112 EKLQIIVEQELSWAF-----RTQGGKYKPKFVYFYSRRCFLFPCKQAAIHQNWADVDY 165
Db 187 GR-----TONAPAFYWRKUTLVTDGKLPDQSEWRAI-----NAGISEAYSGHVE- 234
Qy 166 LNKFFDNGKS-----YSVGRNDKSN--HWNLYVTETDRSTPKGEYIE---DDDETPEVLM 216
Db 235 --PWENNKHLIRWFTISKEDKIDFVYKNIWVMSDDYSWASKKKILELSFTDYNRVGATG 292
Qy 217 TELDPECASKFVCGPEASTTALVEPNEDKGNLGYQMTKRLDEIYVNSAQSDLSFHH 276
Db 293 SSSPTEVASQY--GSDAQ-----MNISDDGTVLIFQ 321
Qy 277 DAFAFT-----CGYSSNMI-----LAEKYVYTLHVTPEKGS-----YASFES 315
Db 322 NAGATPSTGVTLCYDSGNVKNLSSTGSANLSKQYATTKLRMCHGQSYNDNNYCNFTL 381
Qy 316 NIPVFDI-----SQGKQDNLVLLHILNVFOPREFSMTFFTKYQNSQSFQKLLSINES 368
Db 382 SINTIETSYGTSSDCKQ-----FTPPSGS-----AIDLH 412
Qy 369 LPDYIKLDKIV 379
Db 413 LPNYVDLNLALL 423

RESULT 15

US-08-867-941-23
Sequence 23, Application US/08867941
Patent No. 5977337
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:1b
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 944 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-867-941-23
Query Match 4.5%; Score 95; DB 2; Length 944;
Best Local Similarity 18.8%; Pred. No. 2.1;
Matches 75; Conservative 63; Mismatches 152; Indels 110; Gaps 19;
Qy 5 IKELTNHNYI-DHLSATLSDTDAFEGPEKLLIWI-FFPHKKSIITTEKTLRNIGMDRWIEI 63
Db 376 IRDMTEKQYVGTDEAKKFRDKSGVYDGDPRDGLYFVFN-----LEEWKGD 421
Qy 64 LKLVKCEVLSMKTKELDAF-----LL-----SESLFVFDHKLTMKTCGT 104
Db 422 QKLIRGIGLKYSRKTFIDEHRRRRMGLLYRYENKYSNWDKAVLSFD-KQGVATDNN 480
Qy 105 TITLFCLEKLFQIIVEQELSWAFRTTQGGKYKPKFVYFYSRRC-----FLPCKQAAIHQ 157
Db 481 TLKLLNC--AVYPAVD-----KSCRASADKPYSDSDRPHYREQHNVLNASFEKSLKN 531
Qy 158 NWADEVYDNLNKFDPNGKSYSGVGRNDKSNHWNLYVTETDRSTPKGEYIEDDETPEVLM 217
Db 532 KWTQH--HLTGLGYDASNAISRPEQLSHNAARISEYSDYTDKDKYLLG----- 579
Qy 218 ELDPECASKFVCG-PEASTTALVEPNEDKGNLGYQMTKRLDEIYVNSAQSDLSFHH 276
Db 580 --KPEVVEGSCVGYIETLSRKCVPRKINGSNIHISLN-----DRFSIGKYFDFSLGGY 632
Qy 277 DAFAFTPCGYSNNWILAEKYVYTLHVTPEKGSYASFESNIPVFDISQGKQDNLVLLHI 336
Db 633 DRKNFTT--SEELVRSGRYV-----DRSMN-----SGI----- 658
Qy 337 LNVFQP-REFSMTFF-FTKNYQNSQFQKLLSINESLPDYIK 374
Db 659 --VFKNEHESLSYRASSGFTPSFQELFGI-DIYHDYK 695

Search completed: May 11, 2005, 22:53:51
Job time : 29.1959 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:36:02 ; Search time 101.041 Seconds
(without alignments)
1515.788 Million cell updates/sec

Title: US-10-732-923-406

Perfect score: 2118

Sequence: 1 MTVTIKELTNHNYIDHELSA.....KIVYDLDYHLYFMKLQKKI 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118	100.0	396	ADM48038	Adm48038 Polypepti
2	2118	100.0	396	ADS43908	Ads43908 Bacterial
3	709.5	33.5	478	ADG92091	Adg92091 Fungal S-
4	681	32.2	503	Adn20733	Adn20733 Bacterial
5	645	30.5	493	Adm07131	Adm07131 Aspergill
6	645	30.5	493	Adm07012	Adm07012 Aspergill
7	565	26.7	369	Adni19900	Adni19900 Bacterial
8	480	22.7	333	Adde60568	Adde60568 Rat Prote
9	480	22.7	333	Adad48323	Adad48323 Rat Prote
10	480	22.7	333	Adde60572	Adde60572 Rat Prote
11	480	22.7	333	Adad48319	Adad48319 Rat Prote
12	471	22.2	347	ABE61186	ABE61186 Drosophil
13	471	22.2	348	ABAB56589	ABAB56589 Human pro
14	470	22.2	334	AAU84313	AAU84313 Protein A
15	470	22.2	334	ADBE60574	ADBE60574 Human Pro
16	470	22.2	334	ADDA48325	ADDA48325 Human Pro
17	470	22.2	334	ADE60570	ADE60570 Human Pro
18	470	22.2	334	ADDA48321	ADDA48321 Human Pro
19	470	22.2	334	ADN03708	ADN03708 Antipeori
20	470	22.2	334	ADQ828208	ADQ828208 Human 912
21	464	21.9	348	ABG05997	ABG05997 Novel hum
22	434	20.5	368	ADN22644	ADN22644 Bacterial
23	434	20.5	368	ADN22643	ADN22643 Bacterial
24	375.5	17.7	366	3 AAG28816	Aag28816 Arabidops
25	372.5	17.6	400	ADM48040	Adm48040 Polypepti

26	365	17.2	363	5	AAU79674	Aau79674 Cucurbita
27	365	17.2	363	7	ABG75228	Abg75228 Plant wit
28	365	17.2	363	8	ADP90956	Adp90956 Figleaf g
29	365	17.2	363	8	ADR38366	Adr38366 Fig leaf
30	336	15.9	360	2	AAR75006	Aar75006 Tomato S-
31	294	13.9	366	8	ADM48039	Adm48039 Polypepti
32	269.5	12.7	237	7	ABM73860	Abm73860 DNA clone
33	220.5	10.4	309	7	ABM73938	Abm73938 DNA clone
34	190.5	9.0	215	3	AAG28817	Aag28817 Arabidops
35	173.5	8.2	184	8	ADG66385	Adg66385 Novel hum
36	158	7.5	184	3	AAG28818	Aag28818 Arabidops
37	119.5	5.6	196	4	ABG05996	Abg05996 Novel hum
38	111	5.2	1197	4	ABBS8180	Abbs8180 Drosophil
39	111	5.2	1197	7	ADJ37903	Adj37903 D melanog
40	110.5	5.2	900	3	AAB18159	Aab18159 Plasmodiu
41	108.5	5.1	585	7	ADC95867	Adc95867 E. faeciu
42	107.5	5.1	749	5	ABQ04872	Abq04872 LDL recep
43	106.5	5.0	465	2	AAW78921	Aaw78921 Human hae
44	106.5	5.0	1028	4	AAU35923	Aau35923 Helicobac
45	105.5	5.0	655	4	ABG11204	Abg11204 Novel hum

ALIGNMENTS

RESULT 1

ADM48038

ID ADM48038 standard; protein; 396 AA.

XX AC ADM48038;

DT 03-JUN-2004 (first entry)

XX DE Polypeptide sequence #88 useful in producing transgenic plants.

XX KW Yeast; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;

KW osmotic stress; sugar transport; cell cycle pathway; plant height;

KW carbohydrate transport; crop productivity; plant growth;

KW stress resistance; disease resistance; insect resistance; heat tolerance;

KW nitrogen assimilation; water stress tolerance;

KW photosynthetic carbon fixation; virus resistance; gene therapy; gene; ds.

XX OS Saccharomyces cerevisiae.

XX PN US2003233670-A1.

XX PD 18-DEC-2003.

XX PF 04-DEC-2002; 2002US-00310154.

XX PR 04-DEC-2001; 2001US-0337358P.

XX PA (EDGE/) EDGERTON M D.

XX PA (CHON/) CHOMET P S.

XX PA (LACC/) LACCETTI L B.

XX PI Edgerton MD, Chomet PS, Laccetti LB;

XX DR WPI; 2004-061374/06.

XX DR N-PSDB; ADM47670.

XX PT New polynucleotide, useful for manipulating plant protein quality,

XX PT improving plant growth, yield and crop productivity or grain composition

XX PT or producing plants with improved properties.

XX PS Claim 8; SEQ ID NO 456; 144pp; English.

XX CC The present invention relates to polynucleotide sequences, and the

XX CC proteins they encode. The sequences are isolated from a variety of

XX CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,

XX CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The

XX CC polynucleotide and polypeptide sequences of the invention are useful in

XX CC the production of transgenic plants that have improved properties. Also

CC disclosed are methods of producing fertile transgenic plants, preferably
CC maize, with desired phenotypes. The polynucleotide and polypeptide
CC sequences are useful for improving plants by providing protection against
CC osmotic stress, improving altering sugar transport and/or metabolism,
CC modifying the cell cycle pathway, reducing plant height, modifying
CC carbohydrate transport, improving crop productivity, improving plant
CC growth and stress resistance, improving disease resistance, improving
CC insect resistance, improving cold or heat tolerance, improving nitrogen
CC assimilation, improving stalk strength, improving water stress tolerance,
CC improving photosynthetic carbon fixation, improving biotic and abiotic
CC stress resistance, improving resistance to oxidative stress, providing
CC increased vigor, reducing senescence, and conferring virus resistance.
CC The present sequence represents a polypeptide sequence of the invention.
CC Note: The sequence data for this patent is not provided in the printed
CC specification but is obtained in electronic format from the USPTO website
CC at segdata.uspto.gov.

XX SQ Sequence 396 AA;

Query Match 100.0%; Score 2118; DB 8; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.1e-186;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVTIKELTNHNYIDHLSATLSDTAFEGPEKLEIWFPPHKKSIITKTLRNIGMDRW 60
DB 1 MTVTIKELTNHNYIDHLSATLSDTAFEGPEKLEIWFPPHKKSIITKTLRNIGMDRW 60
QY 61 IEILKLVKCEVLSMKTKELDAFLSSSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
DB 61 IEILKLVKCEVLSMKTKELDAFLSSSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
QY 121 ELSWAFRTTGGKYKPKFYPSRRCFLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
DB 121 ELSWAFRTTGGKYKPKFYPSRRCFLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
QY 181 NDKSNHNLVYTTDSTPKGKEYIEDDDTFFVLMTELDPKCAKVFVCCPEASTTALVE 240
DB 181 NDKSNHNLVYTTDSTPKGKEYIEDDDTFFVLMTELDPKCAKVFVCCPEASTTALVE 240
QY 241 PNEDKGNLGYQMTKNTLRDLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNNMILAEKYVYTL 300
DB 241 PNEDKGNLGYQMTKNTLRDLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNNMILAEKYVYTL 300
QY 301 HVTPEKGSVASPESNIPVFDISQKODNLDVLLHLNVFPQPREFSMTFTTKYQNSQFQ 360
DB 301 HVTPEKGSVASPESNIPVFDISQKODNLDVLLHLNVFPQPREFSMTFTTKYQNSQFQ 360
QY 361 KLLSINESLPDYIKLDKIVYDLDYHLYFMKLOKKI 396
DB 361 KLLSINESLPDYIKLDKIVYDLDYHLYFMKLOKKI 396

RESULT 2
ADS43908
ID ADS43908 standard; protein; 396 AA.

XX AC ADS43908;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #22338.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX OS Bacteria.
XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 22338; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at segdata.uspto.gov/sequence.html.

XX SQ Sequence 396 AA;

Query Match 100.0%; Score 2118; DB 8; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.1e-186;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVTIKELTNHNYIDHLSATLSDTAFEGPEKLEIWFPPHKKSIITKTLRNIGMDRW 60
DB 1 MTVTIKELTNHNYIDHLSATLSDTAFEGPEKLEIWFPPHKKSIITKTLRNIGMDRW 60
QY 61 IEILKLVKCEVLSMKTKELDAFLSSSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
DB 61 IEILKLVKCEVLSMKTKELDAFLSSSLFVFDHKLTMKTCGTTTTLFCLEKLFQIVEQ 120
QY 121 ELSWAFRTTGGKYKPKFYPSRRCFLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
DB 121 ELSWAFRTTGGKYKPKFYPSRRCFLFPCKQAAIHQNWADVDYLNKFPDNGKSYSGR 180
QY 181 NDKSNHNLVYTTDSTPKGKEYIEDDDTFFVLMTELDPKCAKVFVCCPEASTTALVE 240
DB 181 NDKSNHNLVYTTDSTPKGKEYIEDDDTFFVLMTELDPKCAKVFVCCPEASTTALVE 240
QY 241 PNEDKGNLGYQMTKNTLRDLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNNMILAEKYVYTL 300
DB 241 PNEDKGNLGYQMTKNTLRDLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNNMILAEKYVYTL 300

Qy 301 HVTPEKWSYASFPESNIPVFDISQKQDNLDVLLHILNVFPREFSMTFTTKYQNSQF 360
 Db 301 HVTPEKWSYASFPESNIPVFDISQKQDNLDVLLHILNVFPREFSMTFTTKYQNSQF 360
 Qy 361 KLSINESLSDYIKLDKIVVDLDDYHLFYMKLQKKI 396
 Db 361 KLSINESLSDYIKLDKIVVDLDDYHLFYMKLQKKI 396

RESULT 3

ADG92091 ID ADG92091 standard; protein; 478 AA.
 AC ADG92091;
 DT 11-MAR-2004 (first entry)
 XX Fungal S-adenosylmethionine decarboxylase (SPE2).
 DE Rice blast fungus; S-adenosylmethionine decarboxylase; SPE2; antibiotic;
 KW antifungal; polyamine biosynthesis; pathogenicity; fungicide; enzyme.
 XX Magnaporthe grisea.
 OS US2003224970-A1.
 XX
 PN 04-DEC-2003.
 XX
 PD 12-MAY-2003; 2003US-00436327.
 XX
 PF 17-MAY-2002; 2002US-0381223P.
 XX
 PR (MAHA/) MAHANTY S.
 XX (HEIN/) HEINIGER R.
 PA (SKAL/) SKALCHUNES A.
 PA (PANH/) PAN H.
 PA (TARP/) TARPEY R.
 PA (SHUS/) SHUSTER J.
 PA (TANZ/) TANZER M M.
 PA (HAME/) HAWER L.
 PA (ADAC/) ADACHI K.
 PA (DEZW/) DEZWAAN T M.
 PA (LOSS/) LO S.
 PA (MONT/) MONTENEGRO-CHAMORRO M V.
 PA (FRAN/) FRANK S.
 PA (DARV/) DARVEAUX B.
 XX Mahanty S, Heiniger R, Skalchunes A, Pan H, Tarpey R, Shuster J;
 PI Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo S;
 PI Montenegro-Chamorro MV, Frank S, Darveaux B;
 XX
 DR WPI; 2004-051922/05.
 DR N-PSDB; ADG92089, ADG92090.
 XX
 PT Identification of test compound as antibiotic e.g. fungicide involves
 PT determining the growth or pathogenicity of fungal organisms having two
 PT forms of a gene involved the polyamine biosynthetic pathway, in the
 PT presence of the compound.
 XX
 PS Claim 41; SEQ ID NO 3; 22pp; English.
 XX
 CC The present invention relates to the isolation of rice blast fungus
 CC (Magnaporthe grisea) S-adenosylmethionine decarboxylase (SPE2), and the
 CC polynucleotide sequences encoding it. Also disclosed is a method for
 CC identifying compounds (e.g. antibiotics, preferably antifungals) that
 CC inhibit SPE2. The enzymes involved in polyamine biosynthesis and
 CC pathogenicity, and the genes encoding the enzymes serve as effective
 CC targets for evaluating antibiotics. The method based on the enzymes and
 CC the genes facilitate screening of effective antibiotics, especially
 CC fungicides. The present sequence represents rice blast fungus SPE2.
 XX
 SQ Sequence 478 AA;

Query Match 33.5%; Score 709.5; DB 8; Length 478;
 Best Local Similarity 35.2%; Pred. No. 2.1e-56;
 Matches 162; Conservative 86; Mismatches 115; Indels 97; Gaps 15;
 Qy 14 IDHLSATLDSTDAFEGPEKLLBIWFPFKKSI---TTEKTLRNIGMDRWIELKLVKCE 70
 Db 23 INHDVAQDLDSGAFEGPEKLELVFAPSPALPLGTKENGKLSVSPDNVEMLDIVNCK 82
 Qy 71 VLSMKTKELDAPLLSESLFVFDHKLTKMTCTGTTTLFCLKLFQI----- 117
 Db 83 ILSVQSSVVDAYLLSESMFVFPKIIILTKCTGTTTLGLAQLLRITAAVDAGFPVFNAS 142
 Qy 118 -VEQELSWAFRTTQGGKYKPFKVFYSRRCFLPFCQKQAAIHQNWADVDYLNKFPDNGKSY 176
 Db 143 SVEDEKAAA-----TPYRVFYSRKNFLFPDRQGRPHRSWKQEVKYLDSMFEGGSAY 193
 Qy 177 SVGRDNKSNHNLIVYTE-----TDRSTPKGKEYI-----EDDETPEVLMTL 219
 Db 194 MVGKMN-GDHWLYMTSPGSTALTPTQTPPAGELMRIPTGLQTAASREDDTLEVLMTDL 252
 Qy 220 DPECASKFVCGPEASTTA-----GQNGRETADIIGHVVGIFKPGFESVTLFEGKGRGEN 251
 Db 253 DPENAKQFYL-EQASALACKQATLAQQAAREEAHAALDKAASTDEQLVSEALTTEGHALGT 311
 Qy 252 QMTKNTRLDEIYVNSA-QDSDLSEFHDAFAFTPCGYSSNMIL-----AEKYYT 299
 Db 312 VVSDTCGLSDVYPKSKYDPDARI-----DAYMEFCGFSANGVVPAPPDATCAQGNHYFT 367
 Qy 300 LHVTPEKWSYASFPESNIPVFDISQKQDNLDVLLHILNVFPREFSMTFTT-KNYQNQS 358
 Db 368 VHTTPEPNCYSASFETNVPG---GQNGRETADIIGHVVGIFKPGFESVTLFEGKGRGEN 424
 Qy 359 FQKL---LSINESLPDYIKLDKIVVDLDDYHLFYMKLQKK 395
 Db 425 GTRADQRLRV-DNVPGYRQDKIVHEFDYDYLVRFYQRE 463
 RESULT 4
 ADN20733 ID ADN20733 standard; protein; 503 AA.
 XX
 AC ADN20733;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #3386.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 OS Bacteria.
 XX
 XX US2003233675-A1.
 PN
 XX 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

QY 246 -----GHNLYQYQMTKNTLDEIYVNSA-QDSLSFHHDAFAFTPCGYSSNMIL----- 292
 DB 312 PPELTTEGHALGTVSVSEACGLSSVYKPKYPSRI-----DAYLFTPCGFSANGVIPPPEG 367
 QY 293 -AEKYYTTLVHTPEKGSYASFPESNIPVFDISQKQDNLDVLLHLNLVNFQPRFSMTFTT 351
 DB 368 KAGTHYFTVHTPEPHCSYASFETNVP---HSQNGQTAGIIKQVVDIFKPGRFSVTLFE 424
 QY 352 KNYQNSQFQ-----KLLSIN-----ESLPDYIKLDKIVVDLDYHL---FYMKLOKK 395
 DB 425 AKPALSQVEDEWKEAKYLAARRTAKMEHVEGYRVRDRIVHDLGDELVFRYYERLDWK 482

RESULT 6
 ADM07012
 ID ADM07012 standard; protein; 493 AA.
 XX
 AC ADM07012;
 XX
 DT 20-MAY-2004 (first entry)
 DE
 XX Aspergillus fumigatus Essential For Growth protein #9.
 XX fungicide; gene therapy; Essential For Growth; EFG; fungal infection.
 XX Aspergillus fumigatus.
 XX WO2003076464-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 13-MAR-2003; 2003WO-IB001374.
 XX
 PR 13-MAR-2002; 2002US-0363543P.
 PR 19-DEC-2002; 2002US-0434407P.
 XX
 PA (FARB) BAYER CROPS SCIENCE SA.
 PA (INSP) INST PASTEUR.
 XX
 PI Grogjean-Cournoyer M, D'enfert CD, Firon A, Villalba F, Lebrun M;
 PI Beffa R;
 XX
 DR WPI; 2003-748377/70.
 DR N-PSDB; ADM07010.
 XX
 PT New nucleic acid encoding an Essential For Growth (EFG) polypeptide,
 PT useful for preparing a composition for treating fungal infection caused
 PT by Aspergillus fumigatus.
 XX
 PS Claim 10; SEQ ID NO 27; 259pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an Essential For Growth
 CC (EFG) polypeptide. The nucleic acid is useful for preparing a composition
 CC for treating fungal infection caused by Aspergillus fumigatus. This
 CC sequence corresponds to a protein of the invention.
 XX
 SQ Sequence 493 AA;

Query Match 30.5%; Score 645; DB 7; Length 493;
 Best Local Similarity 33.9%; Pred. No. 2e-50;
 Matches 162; Conservative 80; Mismatches 120; Indels 116; Gaps 17;

QY 14 IDHLSATLSDAFEGPEKLELWFFPHKKSITTEKT--LRNIGMDRWLEILKVKCEV 71
 DB 25 INYEATQDLSDTNAFEGPEKLELWFFAPSAQELGPAQAGLKVPEIWKMDLDLVNCQV 84
 QY 72 LSMKKTDELDAFLSSESLFVFDHKLTKWCTGTTTLFLCKLEKLFQIVEQBSLWAFRTTQ 131
 DB 85 LSVISSESDVDAYLLSESSMFVPHKILKTKCTGTTLLSGLPRILEIA-----ALFG 135
 QY 132 GKVK-----PFKVFYSRRCLFPCKQAATHQNWADVDVYLNKFPNGKSYSV 178
 DB 136 GFPKSTAPSGISVAAAPYRVFYSRKNFLFPDRQGRPHRSWRDVRTMDKFLNGSAYMI 195

QY 179 GRNDKSNHMLYVTE-----TDRSTPKGK-EYIE-----DDDETEVL 215
 DB 196 GKN-GEHWLYLTERPHTMLTPTSPCAKTEFTETETKVLSPQGAALQTDSEDETLEVL 254
 QY 216 MTELDPECAKFKVCGPEASTALVE-----PNBDK----- 245
 DB 255 MTDLDEENAKQPYL---ENATAVAENRYRNSNEKSHGVDFVFNSTSSDISDFDSGSGQVL 311
 QY 246 -----GHNLYQYQMTKNTLDEIYVNSA-QDSLSFHHDAFAFTPCGYSSNMIL----- 292
 DB 312 PPELTTEGHALGTVSVSEACGLSSVYKPKYPSRI-----DAYLFTPCGFSANGVIPPPEG 367
 QY 293 -AEKYYTTLVHTPEKGSYASFPESNIPVFDISQKQDNLDVLLHLNLVNFQPRFSMTFTT 351
 DB 368 KAGTHYFTVHTPEPHCSYASFETNVP---HSQNGQTAGIIKQVVDIFKPGRFSVTLFE 424
 QY 352 KNYQNSQFQ-----KLLSIN-----ESLPDYIKLDKIVVDLDYHL---FYMKLOKK 395
 DB 425 AKPALSQVEDEWKEAKYLAARRTAKMEHVEGYRVRDRIVHDLGDELVFRYYERLDWK 482

RESULT 7

ADN19900
 ID ADN19900 standard; protein; 369 AA.

XX AC ADN19900;

DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #2553.

XX Recombinant DNA construct; transformed plant; improved plant property;
 cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 pathogen tolerance; pest tolerance; plant disease resistance;
 cell cycle pathway modification; plant growth regulator;
 homologous recombination; seed oil yield; protein yield; carbohydrate;
 nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOV/) CAO Y.
 XX (HINK/) HINKLE G J.
 XX (SLAT/) SLATER S C.
 XX (CHEN/) CHEN X.
 XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 2553; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 promoter functional in a plant cell, where the promoter is positioned to
 provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or by
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX

SQ Sequence 369 AA;

Query Match 26.7%; Score 565; DB 8; Length 369;
 Best Local Similarity 36.1%; Pred. No. 3.2e-43;
 Matches 139; Conservative 75; Mismatches 135; Indels 36; Gaps 13;

QY 14 IDHLSATLSDTAFEGPEKLEIWF-FPHKKSITT-EKT--LRNIGMDRWIEILKLVK 68
 DB 7 VDQENSEEP-NTSFGPEKLEIWFSAPIKTNLSAGEKANLGLKAVSRNDMDMLAQ 65
 QY 69 CEVLSMMKTKELDAFLSESLFVFDHKLTKMTGTTTTLFCLEKLPQIVEQELSWAFRT 128
 DB 66 KVLVSUNSEIDAYLLSESSMFVFAHKILTKGTTTTLASPLRLLEI-----A 115
 QY 129 TQGGKYKPKFVSRRCFLPCKQAAHQWVADEVDYLNKFPNGKSYSGVRNDKSNHW 188
 DB 116 SSVGDFRPLRIFYSRKNFYPERQAPHTSWEEVRYLQFFSGCSYVVGPTNK-NHWH 174
 QY 189 LYVTEDRSTPKGEYEDDDETEPVLMTLDPKASCF-----VCGPEASTALVEP 241
 DB 175 LFDLADYSL-EDSLDPEDETELEVMTDMPERSLQFVAPSLDVVRSAGDDYVREKN 233
 QY 242 NEDKGNLGYQMTKNTRLDEIYVNSAODSLSFHHDFAFTPCGYSSNMILAKEYYYTLH 301
 DB 234 NLSGHLGSVVADESGVRLCSTDKKAVL----DAFQPEPIGFSNNMIYKDR-YATIH 288
 QY 302 VTEPKGHSYASFSNIPVFDISQKQNDLVLLHILNVFQPRFESMTFTTKYVQNSQFQK 361
 DB 289 VTQEHGCSYASFETNVSQFGRSISETIE---KTVKTFGANKFCLTLFOAKGASQ--EK 343
 QY 362 LLSIN-ESLPDYIKLDIVVDLDY 385
 DB 344 HFSAKLKSFSYKKEEFIVDFPGY 368

RESULT 8
 ADE60568
 ID ADE60568 standard; protein; 333 AA.
 XX
 AC ADE60568;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein P17708, SEQ ID NO 6478.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN W02003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.

XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; P17708.
 DR
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 333 AA;

Query Match 22.7%; Score 480; DB 7; Length 333;
 Best Local Similarity 30.9%; Pred. No. 2e-35;
 Matches 117; Conservative 69; Mismatches 137; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLNIGMDRWIEILKLVKCVLSNMKTKEL 80
 DB 1 MEAHFPEGTEKLEIWFVSRQSDASQSGDLRTIPRSEMDVLLKQVCSIIISVTTKDKQ 60
 QY 81 DAFELSESLFVFDHKLTKMTGTTTTLFCLEKLPQIVEQELSWAFRTQGGKYKPF--- 137
 DB 61 EAYVLSSESMFVSKRRFILTCTGTTTTLLKALVPLLLKARD-----YSGFDSI 107
 QY 138 -KVYFRRRCFLFPCKQAAIHONWADEVDYLNKFPNGKSYSGVRNDKSNHNLVVTETDR 196
 DB 108 OSFFYGRKNFMKFSHQYFHRNFQEBIEFLNALFPNGAAYCMGWN-SDCWLYTLDLPE 166
 QY 197 STPKGKEYIBDDDETPEVLMTLDPKASCFVCGPEASTTALVEPNEDKGNHLYQNTKN 256
 DB 167 S-----RVINQPDQTLLEILMSLDPVMDQFYM-----KQGVAKDVRE 206
 QY 257 TRLDIEYVNSAODSLSFHHDFAFTPCGYSSNMILAKEYYYTLHVTPEKWSYASFSN 316
 DB 207 SGIRDLPGSVIDAATL-----FNPCGYSMMGMSDGTGYTHITHTPEFYSVSPETN 258
 QY 317 IPVFDISQKQNDLVLLHILNVFQPRFESMTFTTKYVQNSQFQKLLSINESLPDYIKLD 376

Db 259 -----LSQTSYD--DLIRKVEVFKPGKFTVTLFVN--QSSKCRVTLSSPKIDGFKRLD 309
QY 377 KIVYDLDYHLFYMKLOKX 395
Db 310 COSAMFNDFNVFTSPAKK 328
RESULT 9
ADD48323
ID ADD48323 standard; protein; 333 AA.
XX AC ADD48323;
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX DE Rat Protein AA442105, SEQ ID NO 14021.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX Unidentified.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
DR GENBANK; AAA42105.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Example 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at
CC ffp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 333 AA;
Query Match 22.7%; Score 480; DB 7; Length 333;
Best Local Similarity 30.9%; Pred. NO. 2e-35;
Matches 117; Conservative 69; Mismatches 137; Indels 56; Gaps 10;
QY 22 LDSTDAFEGEKLELWFFPHKKSITT-EKTLNIGMDRWIEILKLVKCEVLNKKTKEL 80
Db 1 MEAHHFEGTEKLELVWFSRQSDASQSGDGLTIPRSEWDLVKDQVCCSIIVTKDRQ 60
QY 81 DAFLLSESLFVFDHKLTKTCTGTTTTLFCLEKLFQIVEQELSWAFFRTTQGGYKPF-- 137
Db 61 EAVLSESSMFVSKRRFILTCTGTTLLKALVLLKLARD-----YSGFDSI 107
QY 138 -KVYISRRCLFPCKQAAIHQNWADVDVYLKPFNDGKSYSGVRNDSKSNHNLVVTETDR 196
Db 108 QSFYISRRKFMKPSHQGYPHRNQEBIEFLNAFPNGAAYCMGRMN-SDCWLYLTLDLPE 166
QY 197 STPKGKEYIEDDDTEFEVLMTLDPKASCFVCGPEASTTALVEPNEDKGNLGYQWTKN 256
Db 167 S-----RVINQPDQTLLELMSLDPAVMDQFYM-----KGVTAQVIRE 206
QY 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAEKYIYTLHVTPEKGMVSPESN 316
Db 207 SGIRDLIPGSVIDATL-----FNPCGYSNMGKSDGTYYTHITPEPEFYVSPETN 258
QY 317 IPVFDISQKQDNLDVLLHLNLNVQPRFSMTFTTKYQNSQKLLSINESLPDYIKLD 376
Db 259 -----LSQTSYD--DLIRKVEVFKPGKFTVTLFVN--QSSKCRVTLSSPKIDGFKRLD 309
QY 377 KIVYDLDYHLFYMKLOKX 395
Db 310 COSAMFNDFNVFTSPAKK 328
RESULT 10
AD860572
ID ADE60572 standard; protein; 333 AA.
XX AC ADE60572;
XX 29-JAN-2004 (first entry)
DT Rat Protein P17708, SEQ ID NO 6482.
XX DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
DR GENBANK; P17708.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

CC cardioactive, immunomodulatory, muscular, vulnery, gastointestinal,
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 348 AA;

Query Match 22.2%; Score 471; DB 3; Length 348;
Best Local Similarity 30.3%; Pred. No. 1.4e-34;
Matches 115; Conservative 70; Mismatches 138; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRNIGMDRWIEILKLVKCEVLMSKTKTEL 80
DB 15 MEAAHFEGETEKLELVFWSRQPPDANOGSGDLRTIPRSEWDILLKDVQCSIIISVTKTDQ 74

QY 81 DAFLLSSSLFVFDHKLTKMTCTGTTTLFCLEKLFQIVEQELSFWAFRTTGGKYKPF--- 137
DB 75 EAYVLSSESMFVSKRRFILTCTGTTLLKALVPLLLKARD-----YSGFDSI 121

QY 138 -KVFSRRCLFPCKQAAIHQWAEVDYLNKFPDNGKSYSGRNDKSNHNLVYVETDR 196
DB 122 QSFYFSRKNFMKPSHQGYPHRNFOEIEFLNAIFPNAGAYCMGRMN-SDCWLYLTLDFFE 180

QY 197 STPKGEYIEDDDTEFVLMTELDPEKASFCVCPGEASTTALVEPNEDKGNLGYQMTKN 256
DB 181 S-----RVISQDQTLIELMSELDPVMDQFYM-----KGVTAQVTR 220

QY 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYYTLHVTPEKGSYASPE 316
DB 221 SGIRDLIPGVIDATM-----FNPCGYSMNGKSGDTGYTWHITPEPEFSYVSPETN 272

QY 317 IPVFDISQKQDNLDVLLHLNVQPREFSMTFTTKYQNSQFQKLLSINESLPDYIKLD 376
DB 273 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKRTVLASPKQIEGFKRLD 323

QY 377 KIVYDLDYHLFYMKLOKK 395
DB 324 QCSAMFNDYNFVFTSFAK 342

RESULT 14
AAU84313
ID AAU84313 standard; protein; 334 AA.
XX
AC AAU84313;
XX
AC AAU84313;
XX
DT 08-MAY-2002 (first entry)
XX
DE Protein AND1 differentially expressed in breast cancer tissue.
XX
KW Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
KW MAI; mitotic activity index; cytostatic.
XX
OS Homo sapiens.
XX
EN WO200210436-A2.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-US023642.
XX
PR 28-JUL-2000; 2000US-0222093P.
XX
PR (BGMH) BRIGHAM & WOMENS HOSPITAL INC.
XX
PA (BAAK/) BAAK J.
XX

PI Baak J, Mutter GL;
XX
DR WP1: 2002-180084/23.
DR N-PSDB; ABK35533.
XX
FT Diagnosing breast cancer comprises determining expression of nucleic acid
XX molecules or expression products that are differentially expressed in
XX normal and malignant tissue.
XX
PS Claim 37; Page 121-122; 219pp; English.
XX
CC The present invention relates to a method for diagnosing breast cancer in
CC a subject suspected of having endometrial cancer. The method comprises
CC determining the expression of a set of human genes or expression products
CC in an endometrial sample suspected of being cancerous. The human genes of
CC the invention are differentially expressed in breast tumours
CC characterised as high or low MAI (mitotic activity index). These sets of
CC genes can be used to discriminate between high and low MAI breast
CC tumours. The invention also provides DNA and protein microarrays for
CC analysing the expression of the human genes and their protein products.
CC The methods and arrays are useful for the diagnosis and prognosis of
CC endometrial cancer, selecting and monitoring treatment regimes, and
CC identification of compounds useful for the treatment of endometrial
CC cancer. AAU84311-AAU84361 represent the human proteins of the invention
CC that are differentially expressed in breast cancer tissue
XX
SQ Sequence 334 AA;

Query Match 22.2%; Score 470; DB 5; Length 334;
Best Local Similarity 30.3%; Pred. No. 1.7e-34;
Matches 115; Conservative 69; Mismatches 139; Indels 56; Gaps 10;

QY 22 LDSTDAFEGPEKLEIWFPHKKSITT-EKTLRNIGMDRWIEILKLVKCEVLMSKTKTEL 80
DB 1 MEAAHFEGETEKLELVFWSRQPPDANOGSGDLRTIPRSEWDILLKDVQCSIIISVTKTDQ 60

QY 81 DAFLLSSSLFVFDHKLTKMTCTGTTTLFCLEKLFQIVEQELSFWAFRTTGGKYKPF--- 137
DB 61 EAYVLSSESMFVSKRRFILTCTGTTLLKALVPLLLKARD-----YSGFDSI 107

QY 138 -KVFSRRCLFPCKQAAIHQWAEVDYLNKFPDNGKSYSGRNDKSNHNLVYVETDR 196
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QY 197 STPKGEYIEDDDTEFVLMTELDPEKASFCVCPGEASTTALVEPNEDKGNLGYQMTKN 256
DB 167 S-----RVISQDQTLIELMSELDPVMDQFYM-----KGVTAQVTR 206

QY 257 TRLDEIYVNSAQSDLSFHHDAFAFTPCGYSSNMILAKEYYTLHVTPEKGSYASPE 316
DB 207 SGIRDLIPGVIDATM-----FNPCGYSMNGKSGDTGYTWHITPEPEFSYVSPETN 258

QY 317 IPVFDISQKQDNLDVLLHLNVQPREFSMTFTTKYQNSQFQKLLSINESLPDYIKLD 376
DB 259 -----LSQTSYD--DLIRKVVVEFKPGKFTVTLFVN--QSSKRTVLASPKQIEGFKRLD 309

QY 377 KIVYDLDYHLFYMKLOKK 395
DB 310 QCSAMFNDYNFVFTSFAK 328

RESULT 15
ADE60574
ID ADE60574 standard; protein; 334 AA.
XX
AC ADE60574;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P17707, SEQ ID NO 6484.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW

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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:40:28 ; Search time 82.4742 Seconds
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Perfect score: 2097

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Searched: 1432185 seqs, 334051727 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2097	100.0	400	15	US-10-310-154-458
2	1958.5	93.4	397	16	Sequence 458, App
3	1715	81.8	450	16	Sequence 47033, A
4	1715	81.8	466	16	Sequence 147033,
5	1687.5	80.5	366	15	US-10-437-963-147475
6	1632	77.8	395	16	Sequence 457, App
7	1632	77.8	554	16	Sequence 142922,
8	1626	77.5	305	15	US-10-425-114-39365
9	1545	73.7	398	16	Sequence 39365, A
10	1538	73.3	289	15	US-10-767-701-46359
11	1517.5	72.4	416	15	US-10-425-114-56960
12	1517.5	72.4	416	15	US-10-425-114-57997
13	1515.5	72.3	422	15	US-10-425-114-67343
					Sequence 36776, A

14	1474	70.3	276	15	US-10-425-114-69727	Sequence 69727, A
15	1357	64.7	392	16	US-10-437-963-128930	Sequence 128930,
16	1354.5	64.6	392	16	US-10-767-701-46141	Sequence 46141, A
17	997	47.5	187	15	US-10-425-114-57416	Sequence 57416, A
18	954	45.5	181	15	US-10-425-114-57901	Sequence 57901, A
19	933.5	44.5	355	15	US-10-424-599-249854	Sequence 249854,
20	933.5	44.5	355	15	US-10-424-599-249859	Sequence 249859,
21	933.5	44.5	356	15	US-10-425-114-46255	Sequence 46255, A
22	933.5	44.5	356	15	US-10-425-114-46648	Sequence 46648, A
23	933	44.5	173	15	US-10-425-114-56901	Sequence 56901, A
24	933	44.5	363	14	US-10-380-913-4	Sequence 4, Appli
25	919.5	43.8	355	15	US-10-424-599-249855	Sequence 249855,
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27	919.5	43.8	360	15	US-10-425-114-46323	Sequence 46323, A
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32	693.5	33.1	203	15	US-10-425-114-58490	Sequence 58490, A
33	667	31.8	224	15	US-10-424-599-205002	Sequence 205002,
34	611	29.1	113	15	US-10-425-114-56995	Sequence 56995, A
35	576.5	27.5	359	16	US-10-437-963-166485	Sequence 166485,
36	466	22.2	368	15	US-10-369-493-5296	Sequence 5296, Ap
37	466	22.2	368	15	US-10-369-493-5297	Sequence 5297, Ap
38	437.5	20.9	369	15	US-10-369-493-2553	Sequence 2553, Ap
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42	420	20.0	334	15	US-10-341-434-20	Sequence 20, Appl
43	420	20.0	334	15	US-10-341-434-127	Sequence 127, App
44	420	20.0	334	17	US-10-753-267-50	Sequence 50, Appl
45	403	19.2	478	15	US-10-436-327-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-310-154-458

Sequence 458, Application US/10310154

Publication No. US20030233670A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

APPLICANT: Chomet, Paul S.

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APPLICANT: Deng, Molian

APPLICANT: Dong, Jinzhao

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APPLICANT: Huang, Shihshien

APPLICANT: Johnson, G. Richard

APPLICANT: Jung, Vincent

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APPLICANT: Lee, Gary

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APPLICANT: Liu, Jingdong

APPLICANT: Lu, Bin

APPLICANT: Luethy, Michael M.

APPLICANT: Lund, Adrian

APPLICANT: Madson, Linda L.

APPLICANT: Malloy, Kathleen A.

APPLICANT: McKiel, Christine L.

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; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manchikanti
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; APPLICANT: Start, William G.
; APPLICANT: Tennesen, Dan
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; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhangguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 458
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Zea mays
; US-10-310-154-458

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Best Local Similarity 100.0%; Pred. No. 9.1e-213;
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Db 61 IVSELSNKDFSDSYLSESSLFYPLKIVIKTCGTTKLLTIPRILELAELSMPAAVKY 120
Qy 121 SRGTFFPGAQAPAPHRFSFEVAALNRYFGGLKSGGNAYVIGDPARPGQKHVYATEYP 180
Db 121 SRGTFFPGAQAPAPHRFSFEVAALNRYFGGLKSGGNAYVIGDPARPGQKHVYATEYP 180
Qy 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
Db 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
Qy 241 GYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSPSEFSVAV 300
Db 241 GYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSPSEFSVAV 300
Qy 301 TIFGGRHAGTWGKALGAEVYDCNNMVEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Db 301 TIFGGRHAGTWGKALGAEVYDCNNMVEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Qy 361 DGENVESAPPMKKDYKLANLLCWEEDADAMEEKAGVLDE 400
Db 361 DGENVESAPPMKKDYKLANLLCWEEDADAMEEKAGVLDE 400

RESULT 2
US-10-767-701-47033
; Sequence 47033, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29

```

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; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 47033
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_367.pgp
; US-10-767-701-47033

Query Match      93.4%; Score 1958.5; DB 16; Length 397;
Best Local Similarity 94.2%; Pred. No. 4.2e-198;
Matches 377; Conservative 7; Mismatches 13; Indels 3; Gaps 2;

Qy 1 MAVLSAADSPVSAIGFEGYKLEITFSEAPVDPHGRLRALSAQIDSVLDLART 60
Db 1 MAVLSAADSPVSAIGFEGYKLEITFSEAPVDPHGRLRALSAQIDSVLDLART 60
Qy 61 IVSELSNKDFSDSYLSESSLFYPLKIVIKTCGTTKLLTIPRILELAELSMPAAVKY 120
Db 61 IVSELSNKDFSDSYLSESSLFYPLKIVIKTCGTTKLLTIPRILELAELSMPAAVKY 120
Qy 121 SRGTFFPGAQAPAPHRFSFEVAALNRYFGGLKSGGNAYVIGDPARPGQKHVYATEYP 180
Db 121 SRGTFFPGAQAPAPHRFSFEVAALNRYFGGLKSGGNAYVIGDPARPGQKHVYATEYP 180
Qy 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
Db 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
Qy 241 GYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSPSEFSVAV 300
Db 241 GYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSPSEFSVAV 300
Qy 301 TIFGGRHAGTWGKALGAEVYDCNNMVEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Db 301 TIFGGRHAGTWGKALGAEVYDCNNMVEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Qy 361 DGENVESAPPMKKDYKLANLLCWEEDADAMEEKAGVLDE 400
Db 361 EGVNMEAPP--VDRKLANLLCW-BEVDAMEEKDGVLE 397

RESULT 3
US-10-437-963-147033
; Sequence 147033, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147033
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_475C.1.pgp
; US-10-437-963-147033

Query Match      81.8%; Score 1715; DB 16; Length 450;
Best Local Similarity 83.3%; Pred. No. 3.1e-172;
Matches 335; Conservative 21; Mismatches 40; Indels 6; Gaps 4;

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Qy	1	MAVLSAADASPVAISAFGEYGEYKRUEITFSEPAVPFVDPHGRLRALSAQIDSVLDIRCT	60
Db	53	MGVLISAADPPPVAISAFGEYGEYKRUEITFSEPAVPFADPGRGLRALSAQIDSVLDIRCT	112
Qy	61	IYVELSNKDFDSVLSSESLFTYPLKIVIKTCGGTKLLLTTPRILEABELSMPLAAVKY	120
Db	113	IYVELSNKDFDSVLSSESLFIYSDKIWIKTCTGGTKLLLTTPRILEABELSMPLAAVKY	172
Qy	121	SRGTFIFPGAQAPAPHRSEFEEVAALNRYFGGLKSGGNAYVIGDPARGQKWHVFYATEYP	180
Db	173	SRGMFIFFPSAQAPAPHRSEFEEVAVLNRYFGHLKSGGNAYVIGDPARGQKWHIYYATQHP	232
Qy	181	EQPMVNLENMCTGLDKKACVPFTKADNONTTCAKEMTKLSGISEIIPEMEICDOPFEPCC	240
Db	233	EQPMVTLENMCTGLDKERASVPFKTSDAGHTSCAKEMTKLSGISDIIPEMEICDOPFEPCC	292
Qy	241	GYSMAIAHGSAFSTTHVTPEDGFSYASVEVWGLDATALSYCDILVKRVLRCFGSPSESVAV	300
Db	293	GYSMAIAHGSAFSTTHVTPEDGFSYASVEVWGFDASTLAYGLDLVKRVLRCFGSPSESVAV	352
Qy	301	TIFGGRGHAGTWGKALGAEVDDCNMNVQEQLPGGGLLVYQSFCAAEED- AVATSPKSVFPH	358
Db	353	TIFGGHGHAGTWAKELNADAYKCNMNVQEQLPCGGGLLIYQSFDAETEDVPVAVGSPKSVLH	412
Qy	359	CFDGENVBSAPPMKKDYKLYLANLILCWEESEADAMEEKAGVLDE	400
Db	413	CFEAEAMNVN- PAPVKREG- KIGULLLPWGE- -DALBENDGVFDE	450

RESULT 4

```

US-10-437-963-147475
; Sequence 147475, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147475
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(466)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_479C.1.pep
US-10-437-963-147475

```

	Query Match	81.8%;	Score 1715;	DB 16;	Length 466;
	Best Local Similarity	83.3%;	Pred. No. 3.2e-172;		
	Matches 335;	Conservative 21;	Mismatches 40;	Indels 6;	Gaps 4;
Qy	1	MAVLSAADAPVSAIGFEGYEKRLIEITFSEAPVFPD	PHRGCLRALSRALSRQAIDSVL	DIARCT	60
Db	69	MGVLSAADPPVSAIGFEGYEKRLIEITFSEAPVFPD	DGRLRALSRQAIDSVL	DIARCT	128
Qy	61	IVSELSNKDPDSYVLSESSFIYPLKVIKTCGTTKLL	LTIPRILEAAELSMPLAAVKY		120
Db	129	IVSELSNKDPDSYVLSESSFIYSDKIVIKTCGTTKLL	LTIPRILEAAGLSMPLAAVKY		188
Qy	121	SRGTFIFPGAQAPHRFSBEVAALNRYFGGLKSGGNAY	IGDPAFGQKWHVFATAYEP		180

[illegible]

RESULT 5

US-10-310-154-457
Sequence 457, Application US/10310154
Publication No. US20030233670A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupalli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deng, Molian
APPLICANT: Dong, Jinzhao
APPLICANT: Duff, Stephen M.
APPLICANT: Galligan, Meghan M.
APPLICANT: Hinchey, Brenda S.
APPLICANT: Huang, Shihshieh
APPLICANT: Johnson, G. Richard
APPLICANT: Jung, Vincent
APPLICANT: Kretzmer, Keith A
APPLICANT: Laccetti, Lucille B.
APPLICANT: Lai, Chao-Qiang
APPLICANT: Lee, Gary
APPLICANT: Lin, Jie-Yi
APPLICANT: Liu, Jingdong
APPLICANT: Lu, Bin
APPLICANT: Luethy, Michael M.
APPLICANT: Lund, Adrian
APPLICANT: Madson, Linda L.
APPLICANT: Malloy, Kathleen A.
APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310.154

```

; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 457
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Zea mays
US-10-310-154-457

Query Match      80.5%; Score 1687.5; DB 15; Length 366;
Best Local Similarity 85.0%; Pred. No. 1.8e-169;
Matches 328; Conservative 7; Mismatches 20; Indels 31; Gaps 2;

Qy 1 MAVLSAADASPVSAGIFEGYKLEITFSEAPVDPVDPHGRLRALSPQAQDSVLDLARCT 60
Db 1 MAVLSAADASPVSAGIFEGYKLEITFSEAPVDPVDPHGRLRALSPQAQDSVLDLARCT 60
Qy 1 IVSELSNKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPLEAAVKY 120
Db 1 IVSELSNKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPLEAAVKY 120
Qy 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPAKPGQKWHVYATEYP 180
Db 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPAKPGQKWHVYATEYP 180
Qy 181 EQPMVNLNEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
Db 181 EQPMVNLNEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
Qy 241 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGLDATALSYGDLVKVRLRCFGPSEFSVAV 300
Db 241 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGLDATALSYGDLVKVRLRCFGPSEFSVAV 300
Qy 301 TIFGGRGAGTGWKALGAEVYDCNNMVEQELPGGLLVYQSFCAAEDAVATSPKSVPHCF 360
Db 301 TIFGGRGAGTGWKALGAEVYDCNNMVEQELPGGLLVYQSFCAAEDAVATSPKSVPHCF 360
Qy 361 DGENVESAPPMKDYKLANLLCWEEADAMEEKAG 396
Db 361 DGENVESAPPMKDYKLANLLCWEEADAMEEKAG 396
Qy 361 ADENTEKAGK-----MEALYMED--DAVEEDIG 386
Db 361 ADENTEKAGK-----MEALYMED--DAVEEDIG 386

RESULT 7
US-10-437-963-142921
; Sequence 142921, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142921
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43880C.1.pap
US-10-437-963-142921

Query Match      77.8%; Score 1632; DB 16; Length 554;
Best Local Similarity 79.3%; Pred. No. 2.6e-163;
Matches 314; Conservative 26; Mismatches 46; Indels 10; Gaps 2;

Qy 1 MAVLSAADASPVSAGIFEGYKLEITFSEAPVDPVDPHGRLRALSPQAQDSVLDLARCT 60
Db 72 MAVLSAADASPVSAGIFEGYKLEITFSEAPVDPVDPHGRLRALSPQAQDSVLDLARCT 131
Qy 61 IVSELSNKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPLEAAVKY 120
Db 132 IVSELSNKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPLEAAVKY 191
Qy 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPAKPGQKWHVYATEYP 180
Db 192 SRGTFFPGAQAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPAKPGQKWHVYATEYP 251

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; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 457
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Zea mays
US-10-310-154-457

Query Match      80.5%; Score 1687.5; DB 15; Length 366;
Best Local Similarity 85.0%; Pred. No. 1.8e-169;
Matches 328; Conservative 7; Mismatches 20; Indels 31; Gaps 2;

Qy 1 MAVLSAADASPVSAGIFEGYKLEITFSEAPVDPVDPHGRLRALSPQAQDSVLDLARCT 60
Db 1 MAVLSAADASPVSAGIFEGYKLEITFSEAPVDPVDPHGRLRALSPQAQDSVLDLARCT 60
Qy 61 IVSELSNKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPLEAAVKY 120
Db 59 -----KIVIKTCGTTKLLLTIPRILELAELSMPLEAAVKY 93
Qy 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPAKPGQKWHVYATEYP 180
Db 94 SRGTFFPGAQAPHRFSFSEVAALNRYFGGLKSGGNAYVIGDPAKPGQKWHVYATEYP 153
Qy 181 EQPMVNLNEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
Db 154 EQPMVNLNEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 213
Qy 241 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGLDATALSYGDLVKVRLRCFGPSEFSVAV 300
Db 214 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGLDATALSYGDLVKVRLRCFGPSEFSVAV 273
Qy 301 TIFGGRGAGTGWKALGAEVYDCNNMVEQELPGGLLVYQSFCAAEDAVATSPKSVPHCF 360
Db 274 TIFGGRGAGTGWKALGAEVYDCNNMVEQELPGGLLVYQSFCAAEDAVATSPKSVPHCF 333
Qy 361 DGENVESAPPMKDYKLANLLCWEEADAMEEKAG 396
Db 334 DGENVESAPPMKDYKLANLLCWEEADAMEEKAG 355

RESULT 6
US-10-437-963-142922
; Sequence 142922, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142922
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43881C.1.pap
US-10-437-963-142922

Query Match      77.8%; Score 1632; DB 16; Length 395;
Best Local Similarity 79.3%; Pred. No. 1.6e-163;
Matches 314; Conservative 26; Mismatches 46; Indels 10; Gaps 2;

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Qy 181 EQPMVNLEMCMWTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFEPC 240
Db 252 EQPVVLEMCMTGLDKKKASVFFKTSADGHTTAKEMTKLSGISDIPEMEVCDFDFEPC 311
Qy 241 GYSNNAIHGSAFSTIHTVPDGFSGYASVEYVWGLDATALSYGDLVKRVLRCFGSERSVAV 300
Db 312 GYSNNAIHGSAFSTIHTVPDGFSGYASVEYVWGLDATALSYGDLVKRVLRCFGSERSVAV 371
Qy 301 TIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 360
Db 372 TIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVPHCF 431
Qy 361 DGENVESAPPMKKOYKLANLLCWEEADAMEEKAG 396
Db 432 ADENTEKAGK-----MEALYWED--DAVEEIDG 457

RESULT 8
US-10-425-114-39365
; Sequence 39365, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39365
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700074853_FLI.pbp
US-10-425-114-39365
Query Match 77.5%; Score 1626; DB 15; Length 305;
Best Local Similarity 100.0%; Pred. No. 4.5e-163;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 96 KLLITTPRIELEAELSMPAAVKYSGTTFPGQAQAPAPHRSPSEVAALNRYFGGLKSG 155
Db 1 KLLITTPRIELEAELSMPAAVKYSGTTFPGQAQAPAPHRSPSEVAALNRYFGGLKSG 60
Qy 156 GNAVYIGDPAKPGQKWHVFVATEYPEOPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAK 215
Db 61 GNAVYIGDPAKPGQKWHVFVATEYPEOPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAK 120
Qy 216 EMTKLSGISIIPEMEICDFDFEPCGYSNNAIHGSAFSTIHTVPDGFSGYASVEYVWGLDA 275
Db 121 EMTKLSGISIIPEMEICDFDFEPCGYSNNAIHGSAFSTIHTVPDGFSGYASVEYVWGLDA 180
Qy 276 TALSVDLVRKVLRCFGPSFSFSAVATTIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGG 335
Db 181 TALSVDLVRKVLRCFGPSFSFSAVATTIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGG 240
Qy 336 LLVYQSFCAAEADAVATSPKSVPHCFDGENVESAPPMKKOYKLANLLCWEEADAMEEKA 395
Db 241 LLVYQSFCAAEADAVATSPKSVPHCFDGENVESAPPMKKOYKLANLLCWEEADAMEEKA 300
Qy 396 GVLDE 400
Db 301 GVLDE 305

RESULT 9
US-10-767-701-46359
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; Sequence 46359, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46359
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CL511_1.pbp
US-10-767-701-46359
Query Match 73.7%; Score 1545; DB 16; Length 398;
Best Local Similarity 76.5%; Pred. No. 2.6e-154;
Matches 302; Conservative 36; Mismatches 47; Indels 10; Gaps 3;
Qy 1 MAVLSAADAS--PVSAIGFEGYEKRLKITFSEAPVFPVDPHGRGLRALSRQAQIDSVLDLAR 58
Db 1 MAVLQVAAAAAPPVSAIGFEGYEKRLKITFSEAPVFPVDPHGRGLRALSRQAQIDSVLDLAR 60
Qy 59 CTIVSELNKPDSYVLSSESLFIYPLKIVIKTCGTTKLLITPRIELEAELSMPAAV 118
Db 61 CTIVSELNKPDSYVLSSESLFIYPLKIVIKTCGTTKLLITPRIELEAELSMPAAV 120
Qy 119 KYSRGTFIPGAQAPAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKPGQKWHVFVATE 178
Db 121 KYSRGTFIPGAQAPAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKPGQKWHVFVATE 180
Qy 179 YPEQPMVNLEMCMTGLDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFE 238
Db 181 HPEEPVVTLEMCMTGLDKKKASVFFKTSADGYTSCAKEMTKLSGISDIPEMEICDFDFE 240
Qy 239 PCGYSNNAIHGSAFSTIHTVPDGFSGYASVEYVWGLDATALSYGDLVKRVLRCFGPSFSV 298
Db 241 PCGYSNNAIHGSAFSTIHTVPDGFSGYASVEYVWGLDATALSYGDLVKRVLRCFGPSFSV 300
Qy 299 AVTIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVFH 358
Db 301 AVTIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGGLLVYQSFCAAEADAVATSPKSVFH 360
Qy 359 CFDPGENVESAPPMKKOYKLANLLCWEEADAMEE 393
Db 361 DFAGDIVKPG-----DSGEADGPCW--EADAVDE 387

RESULT 10
US-10-425-114-56960
; Sequence 56960, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56960
; LENGTH: 289
; TYPE: PRT
```

```
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17089E06_FLI.pep
US-10-425-114-56960

Query Match      73.3%; Score 1538; DB 15; Length 289;
Best Local Similarity 99.3%; Pred. No. 8.7e-154;
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 112 SMPAAVYKSRGTFFPGAQAPHRSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKW 171
Db 1 SMPAAVYKSRGTFFPGAQAPHRSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKW 60

Qy 172 HVFYATYEPQPMVNLNEMCTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPME 231
Db 61 HVFYATYEPQPMVNLNEMCTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPME 120

Qy 232 ICDFDPEPCGYSMNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCF 291
Db 121 ICDFDPEPCGYSMNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCF 180

Qy 292 GPSEFSVAVTIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVAT 351
Db 181 GPSEFSVAVTIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVAT 240

Qy 352 SPKSVFHCFCGDNVESAPPKMKDYKLANLLCWEEDAMEEKAGVLDE 400
Db 241 SPKSVFHCFCGDNVESAPPKMKDYKLANLLCWEEDAMEEKAGVLDE 289

RESULT 11
US-10-425-114-57997
; Sequence 57997, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57997
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17023A12_FLI.pep
US-10-425-114-57997

Query Match      72.4%; Score 1517.5; DB 15; Length 416;
Best Local Similarity 74.8%; Pred. No. 2.2e-151;
Matches 297; Conservative 29; Mismatches 52; Indels 19; Gaps 3;

Qy 1 MAVLSAADASPVSAIGPEGYEKLEITFSEAPVDPHGRLRALSAQAIDSVLDLACT 60
Db 24 MAVLQAAAPPVSVIGFEGEKELEISFSEAPVLADPSGRLRALSAQAIDSVLDLACT 83

Qy 61 IVSELSNKDFSDSVLSESSLFVYPLKIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKY 120
Db 84 IVSELSNDDFSDSVLSESSLFVYPIKIVIKTCGTTKLLLTIPRILELAELLLPLAAVKY 143

Qy 121 SRGTFFPGAQAPHRSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKWVFYATEYP 180
Db 144 SRGTFFPGAQAPHRSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKWVFYAAEHP 203

Qy 181 EQPMVNLNEMCTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDPEPC 240
Db 204 EEPVVTLEMCMTGLDKKASVFFKTTADGYSLCAKEMTKLSGISEIIPMEICDFDPEPC 263

Qy 241 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGSEFSVAV 300
Db 264 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGTEFSVTV 323

Qy 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHCFC 360
Db 324 TIFGDRNNAKTWTKLDAEAYACSNMVEQVLPFGGLLIYOSFTVTAETTHGSPRSVLHDF 383

Qy 361 DGENV-----ESAPPPMKDYKLANLLCWEEDAMEE 393
Db 384 AGDIVKNRSESDAP-----W--EADAVDE 405
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Db 204 EEPVVTLEMCMTGLDKKASVFFKTTADGYSLCAKEMTKLSGISEIIPMEICDFDPEPC 263
Qy 241 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGSEFSVAV 300
Db 264 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGTEFSVTV 323
Qy 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHCFC 360
Db 324 TIFGDRNNAKTWTKLDAEAYACSNMVEQVLPFGGLLIYOSFTVTAETTHGSPRSVLHDF 383
Qy 361 DGENV-----ESAPPPMKDYKLANLLCWEEDAMEE 393
Db 384 AGDIVKNRSESDAP-----W--EADAVDE 405

RESULT 12
US-10-425-114-67343
; Sequence 67343, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67343
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB4767-001-F3_FLI.pep
US-10-425-114-67343

Query Match      72.4%; Score 1517.5; DB 15; Length 416;
Best Local Similarity 74.8%; Pred. No. 2.2e-151;
Matches 297; Conservative 29; Mismatches 52; Indels 19; Gaps 3;

Qy 1 MAVLSAADASPVSAIGPEGYEKLEITFSEAPVDPHGRLRALSAQAIDSVLDLACT 60
Db 24 MAVLQAAAPPVSVIGFEGEKELEISFSEAPVLADPSGRLRALSAQAIDSVLDLACT 83

Qy 61 IVSELSNKDFSDSVLSESSLFVYPLKIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKY 120
Db 84 IVSELSNDDFSDSVLSESSLFVYPIKIVIKTCGTTKLLLTIPRILELAELLLPLAAVKY 143

Qy 121 SRGTFFPGAQAPHRSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKWVFYATEYP 180
Db 144 SRGTFFPGAQAPHRSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKWVFYAAEHP 203

Qy 181 EQPMVNLNEMCTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDPEPC 240
Db 204 EEPVVTLEMCMTGLDKKASVFFKTTADGYSLCAKEMTKLSGISEIIPMEICDFDPEPC 263

Qy 241 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGSEFSVAV 300
Db 264 GYSNNAIHGSAFSTIHVTPEDGFSYASVEVMGLDATALSYGDLVKRVLRCFCGTEFSVTV 323

Qy 301 TIFGGRGHAGTWKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFHCFC 360
Db 324 TIFGDRNNAKTWTKLDAEAYACSNMVEQVLPFGGLLIYOSFTVTAETTHGSPRSVLHDF 383

Qy 361 DGENV-----ESAPPPMKDYKLANLLCWEEDAMEE 393
Db 384 AGDIVKNRSESDAP-----W--EADAVDE 405
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RESULT 13
US-10-425-114-36776
; Sequence 36776, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36776
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-020-E2_FLI.pep
US-10-425-114-36776

Query Match 72.3%; Score 1515.5; DB 15; Length 422;
Best Local Similarity 74.7%; Pred. No. 3.7e-151;
Matches 298; Conservative 31; Mismatches 49; Indels 21; Gaps 4;

QY 1 MAVLSAADAS--PVSAIGFEGYKRLIETPSEAPVFDVPHGRGLRALSRQAIDSVDLRL 58
DB 28 MAVLVAANAAPPVSVIGFEGFKRLIETPSEAPVLDPSGRGLRALSRQAIDSVDLRL 87
QY 59 CTIVSELSNKFDSYVLSSESLFYPLKIVIKTCGTTKLLTIPRILELAELSMPAAV 118
DB 88 CTIVSELSNKFDSYVLSSESLFYPLKIVIKTCGTTKLLTIPRILELAELSMPAAV 147
QY 119 KYSRGTFIFPGAOPAPHRFSFEVAALNRYFGLKSGGNAYVIGDPAKQKWHVYATE 178
DB 148 KYSRGTFIFPGAOPAPHRFSFEVAALNRYFGLKSGGNAYVIGDPAKQKWHVYAAE 207
QY 179 YPQPWNVLEMCMGTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPE 238
DB 208 HPEEPVVTLEMCMGTGLDKKACVFFKTTADGYSILCAKEMTKLSGISEIIPMEICDFPE 267
QY 239 PCGYSNATHGSFSTHVTPEDFGSYASVEVMGLDATALSYGDLVKRVLRCFPGSEFSV 298
DB 268 PCGYSNATHGSFSTHVTPEDFGSYASVEVMGLDATALSYGDLVKRVLRCFPGTEFSV 327
QY 299 AVTIFGGRHAGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFH 358
DB 328 AVTIFGDRNAGTWGKALDAEAYACSNMVEQVLPFGGLLIYQSFVTAETHGSPRSVLH 387
QY 359 CFQGENV----ESAPPPMKDYKLANLLCWEEADAMEE 393
DB 388 DFAGDIVKRNSEDAP-----W--EADAVDE 411

RESULT 14
US-10-425-114-69727
; Sequence 69727, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69727
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17199H04_FLI.pep
US-10-425-114-69727

Query Match 70.3%; Score 1474; DB 15; Length 276;
Best Local Similarity 99.3%; Pred. No. 4.8e-147;
Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 125 FIFPGAOPAPHRFSFEVAALNRYFGLKSGGNAYVIGDPAKQKWHVYATEYEPQPM 184
DB 1 FIFPGAOPAPHRFSFEVAALNRYFGLKSGGNAYVIGDPAKQKWHVYATEYEPQPM 60
QY 185 VNLEMCMGTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSM 244
DB 61 VNLEMCMGTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSM 120
QY 245 NAIHGSFSTHVTPEDFGSYASVEVMGLDATALSYGDLVKRVLRCFPGSEFSVAVTIFG 304
DB 121 NAIHGSFSTHVTPEDFGSYASVEVMGLDATALSYGDLVKRVLRCFPGSEFSVAVTIFG 180
QY 305 GRGHAGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFCHPDGEN 364
DB 181 GRGHAGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAAEADAVATSPKSVFCHPDGEN 240
QY 365 VESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE 400
DB 241 VESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE 276

RESULT 15
US-10-437-963-128930
; Sequence 128930, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128930
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31236C.1.pep
US-10-437-963-128930

Query Match 64.7%; Score 1357; DB 16; Length 392;
Best Local Similarity 67.6%; Pred. No. 2e-134;
Matches 267; Conservative 47; Mismatches 71; Indels 10; Gaps 5;

QY 4 LSAAD---ASPVSAIGFEGYKRLIETPSEAPVFDVPHGRGLRALSRQAIDSVDLRLACT 60
DB 3 MSLAWSGAPASPIGFEYKRLIETLSDAPVFDVPCGGLRALSRQAIDSVDLRLACT 62
QY 61 IVSELSNKFDSYVLSSESLFYPLKIVIKTCGTTKLLTIPRILELAELSMPAAV 120
DB 63 IVSHLSNKFDSYVLSSESLFYPLKIVIKTCGTTKLLTIPRILELAELSMPAAV 122


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QY 121 SRGTFIPGAOPAPHSFSEEEVAALNRYFGGLKSGGNAYVIGDPAPRGOKWHVYATEYP 180
Db 123 SRGMFIPGAQSPHRSFLEEEVSLNSFFGGLKSGGNAYVIGDAFKPKKWHVYATEEP 182
QY 181 EQPMVNLEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
Db 183 EQPMVTLEMCMTGLDAKAEVFFKSTDSGSSAKEMTFSGISEIIPEMEICDFDFEPC 242
QY 241 GYSMNAIHGSAFSTIHVTPEDEGFSYASYEVMGLDATALSYGDLVKVLRFCFGPSEFSVAV 300
Db 243 GYSMNGIYGPAVSTIHVTPEEGFSYASYEAMNFPSSLVYDDLKVKLACFCPSDFSVA 302
QY 301 TIFGGRGHAGTGWKALGAEVYDCNNVVEQLPGGGLLVYOSFCAAEADAVATSPKSVFHC 360
Db 303 TIFGGRGHAGTGWKALGAEVYDCNNVVEQLPGGGLLVYOSFCAAEADAVATSPKSVFHC 360
QY 361 DGENVESAPPPMKDYKLANLLCWESEADAMEEKA 395
Db 359 DGNWSDGA-EMVAKSKEMS--VCWEGEKAACKYDA 390

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Search completed: May 11, 2005, 22:57:58
Job time : 83.4742 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:39:42 ; Search time 26.4605 Seconds
(without alignments)
1128.461 Million cell updates/sec

Title: US-10-732-923-408

Perfect score: 2097
Sequence: 1 MAVLSAADSPVSAIGFEGY.....LLCWEEDAMEKAGVLDE 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
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4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	20.2	348	4	US-09-949-016-10038 Sequence 10038, A
2	420	20.0	334	4	US-09-917-254-54 Sequence 54, Appl
3	406.5	19.4	424	4	US-09-248-796A-18169 Sequence 18169, A
4	101.5	4.8	350	4	US-09-902-540-11867 Sequence 11867, A
5	100.5	4.8	410	4	US-09-010-877-2 Sequence 2, Appl
6	94	4.5	1165	1	US-07-828-788A-14 Sequence 14, Appl
7	94	4.5	1165	1	US-08-356-034-4 Sequence 4, Appl
8	94	4.5	1165	3	US-08-933-891-4 Sequence 4, Appl
9	94	4.5	1165	4	US-09-521-344-4 Sequence 4, Appl
10	94	4.5	1165	4	US-09-837-961A-4 Sequence 4, Appl
11	94	4.5	1165	5	PCT-US92-11337-14 Sequence 14, Appl
12	94	4.5	1165	6	5188960-4 Patent No. 5188960
13	94	4.5	1165	6	5188960-4 Patent No. 5188960
14	91.5	4.4	270	4	US-08-773-368-1 Sequence 1, Appl
15	91.5	4.4	270	3	US-09-199-887-1 Sequence 1, Appl
16	91.5	4.4	502	4	US-09-489-039A-13971 Sequence 13971, A
17	91	4.3	1165	3	US-09-176-320-6 Sequence 6, Appl
18	89.5	4.3	621	4	US-09-537-120-2 Sequence 2, Appl
19	89	4.2	288	4	US-09-270-767-43786 Sequence 43786, A
20	89	4.2	2559	4	US-09-902-540-16112 Sequence 16112, A
21	87.5	4.2	499	4	US-09-543-681A-6892 Sequence 6892, Ap
22	87.5	4.2	856	4	US-09-328-352-7255 Sequence 7255, Ap
23	87	4.1	833	4	US-09-583-110-4098 Sequence 4098, Ap
24	87	4.1	862	4	US-09-107-433-3190 Sequence 3190, Ap
25	86	4.1	795	3	US-07-741-453A-55 Sequence 55, Appl
26	85	4.1	568	4	US-09-902-540-9948 Sequence 9948, Ap
27	85	4.1	634	4	US-09-248-796A-19513 Sequence 19513, A

28	85	4.1	662	4	US-09-543-681A-7467 Sequence 7467, Ap
29	85	4.1	833	2	US-08-844-086-2 Sequence 2, Appl
30	85	4.1	833	3	US-09-018-211-2 Sequence 2, Appl
31	85	4.1	1472	4	US-09-032-438C-119 Sequence 119, App
32	84.5	4.0	666	4	US-09-134-000C-5066 Sequence 5066, Ap
33	84.5	4.0	850	4	US-09-515-181A-3 Sequence 3, Appl
34	84	4.0	331	4	US-09-710-279-874 Sequence 874, App
35	84	4.0	331	4	US-09-710-279-2244 Sequence 2244, Ap
36	84	4.0	342	3	US-09-134-001C-5198 Sequence 5198, Ap
37	84	4.0	607	2	US-08-472-534-5 Sequence 5, Appl
38	84	4.0	607	4	US-09-583-110-4651 Sequence 4651, Ap
39	84	4.0	612	4	US-09-107-433-3621 Sequence 3621, Ap
40	83.5	4.0	766	4	US-09-463-238-6 Sequence 6, Appl
41	82.5	3.9	481	3	US-09-537-357-7 Sequence 7, Appl
42	82.5	3.9	1054	4	US-09-693-542-87 Sequence 87, Appl
43	82	3.9	321	4	US-09-498-520A-18 Sequence 18, Appl
44	81	3.9	251	4	US-09-270-767-48514 Sequence 48514, A
45	81	3.9	308	4	US-09-902-540-14965 Sequence 14965, A

ALIGNMENTS

RESULT 1
US-09-949-016-10038
; Sequence 10038, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10038
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10038

Query Match	20.2%	Score 424;	DB 4;	Length 348;
Best Local Similarity	36.9%	Pred. No. 3.5e-39;		
Matches 109;	Conservative 48;	Mismatches 114;	Indels 24;	Gaps 9;
QY	17	FEYKRLITFSEAFVFDPHGRGRALSRAGIDSVLDRCTIVSELNKNQFDSVLS	76	
DB	21	FEGETLEWFSRQOPDANQSGDLRTIPRSEWDILLKDVQCSIIIVTKDQEAIVLS	80	
QY	77	ESSLIYPLKIVIKTCGTTKLLITIPRIELAEELS--MPLAAVKYSGCTFIEPQAQAP	134	
DB	81	ESSMFYKSRFILKTCGTTLLKALVPLKLARDYSGFDSIQFFYKRNKMPKSHQGY	140	
QY	135	HRFSFEVAAALNRYFGGLKSGGNAYVIGOPARQKQWHVFYATEYDE----OPMVNLEM	189	
DB	141	HRNFQEIIFLNAIF-----PNGAAYCMG---RNNSDCWLYTLDFPESRVISQPDQLEI	193	
QY	190	CMTGLDKKCAVFEKTNADGNTTCAKEMTKLSIGSIIPMEIICDFEPCGYSMAIHG	249	
DB	194	LMSELDPAVMQPYM--KDGVT--AKDVTRESGIRDLIPGSDVATMNFPCGYSNMGKS	249	
QY	250	-SAFSITHITPEPCFYSAYEVWGLDATALSYGDLKVKVLCFCGPSEFSVAVIF	303	
DB	250	DGTWYTHITPEPEFSYVSFET---NLSTSYDILLIRKVVVEPKPGKF--VTTLF	299	

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RESULT 2
US-09-917-254-54
; Sequence 54, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 54
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-54

Query Match      20.0%; Score 420; DB 4; Length 334;
Best Local Similarity 36.6%; Pred. No. 9.4e-39;
Matches 108; Conservative 48; Mismatches 115; Indels 24; Gaps 9;

QY 17 FEYGEKLEITFEAPVFDVPHGRGLRALSRQAIDSVLDLACTIVSELSNKFDSYVLS 76
DQ 7 FEYGEKLEITFEAPVFDVPHGRGLRALSRQAIDSVLDLACTIVSELSNKFDSYVLS 66
QY 77 ESSLFTYPLKIVTKTCTGTTKLLTIPRILELAELS--MPLAAVKYSRGTFFIFGQAPAP 134
DQ 67 ESSMFWKRRFIIKTCGTTLLKALVPLLLKARDYSGFDSIQFFYSRKNFMRPSHQGY 126
QY 135 HRSFSEVAALNRYFGGLKSGNAYVIGDPAFGQKWHVFYATEYPE-----QPMVNLEM 189
DQ 127 HRNFQEIPEFLNAIF---PNGAGYCMG---RNSDCWLYTLDFPESRVISQPDQLEI 179
QY 190 CWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFFPEPCGYSMAIHG 249
DQ 180 LMSGLDPAVNDQFYM--KDGVT--AKDVTRESGIRDLIPGSVIDATMFPNPGYSMNGMS 235
QY 250 -SAFSTHTVTPEDGFSYASVEVMGLDATALSYGLVKVLRCLFCGPFSEFSVAVTIF 303
DQ 236 DGTWTHTIHTPEFSVSFET---NLSQTSYDLDLRKVVVEFKPGKF--VTTLF 285

RESULT 3
US-09-248-796A-18169
; Sequence 18169, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18169
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18169

Query Match      19.4%; Score 406.5; DB 4; Length 424;
Best Local Similarity 32.2%; Pred. No. 4.8e-37;
Matches 110; Conservative 59; Mismatches 99; Indels 75; Gaps 12;

QY 13 SAIGFEGYKRLITFSE-----APVFDVPHGRGLRALSRQAIDSVLDLACTIVSELSN 68
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Db 61 STHAFEGPEKLLIWFYSEKELSPI-----NLRDIKPTDWIELNLVHCEVLKSYSSN 113
QY 69 DFDSYVLSSESLFIYPLKIVTKTCTGTTKLLTIPRILE-LABEL-----SMLA 116
DQ 114 LCDAPLSSSLFVFPFKIILKTCGTTTTLACLDLLFETVKNELLQNEGLKATFQSKNIY 173
QY 117 AVKYSRGTFFPCAQAPHRSPSEEEVAALNRYFGGLKSGNAYVIGDPAFGQKWHVFY- 175
DQ 174 QIFYSRRSPFMDPRQIHVHGNWQEEVKLLNQYF---NNGKSYIVGN---NTNWHLYVG 225
QY 176 -----ATEYPEQPMVN--LEMCMTGLDKKACVFFKTNADGNTT----- 212
DQ 226 GNGTKNPNVASTTTTTTTPVNDCTLEIIMTQLSLEASQOFTYTRKPGDTAIDSNHDLGH 285
QY 213 -CAKEMTKLSGISEII-----PEMEICD-FDFEPCGYSMAIHGSAFSTIH 256
DQ 286 DLQGEILKQTLGNELPFKFKKQPTMPGLSSSPIKEIHDGFAFTPCGFSNSINESNYTIIH 345
QY 257 VTPEDGFSYASVEVMGLDATALSYGLVKVLRCLFCGPFSEFSV 298
DQ 346 VTPEGWSYASFETNMIG---DYKAIVDKCINVPQPGQPMV 383

RESULT 4
US-09-902-540-11867
; Sequence 11867, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11867
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11867

Query Match      4.8%; Score 101.5; DB 4; Length 350;
Best Local Similarity 21.2%; Pred. No. 0.018;
Matches 51; Conservative 28; Mismatches 97; Indels 65; Gaps 9;

QY 171 WH---VFYATEYPEQPMVNLEMCMWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEII 227
DQ 37 WHVSNVFS-----QPQIDLAAQLTWSGLSRAFFCNSGAEANEALLKTRKVMKDRGTP 91
QY 228 PEMEICDPEPCGYSMAIHGSAFSTIHTVTPEDGFSYASVEVMGLDATALSYGLVKRV 287
DQ 92 EREFEVSFD-----SSPHGRTLATVATGAKYQ-KGFEPLPAGFTHPVPGDL-EAV 141
QY 288 LRCFGPSEFSVAVTIFGGRG-----HA-----GTWKGAL 316
DQ 142 RKAVGATAAILVEPIQEGGVERMAPLGLVLGRLALCDEHGLLLLVDEVQTMGRTKGPF 201
QY 317 GAELYDCNNMVEQLP-----GGGLLVYOSFCAAEADAVATSPKSVFHCFDGENVES 367
DQ 202 GF-----MHGIVPDGISVAKALGNLPIGAMLCKEELGASLITPGTHGSTFGGNDVAA 254
QY 368 A 368
DQ 255 A 255

RESULT 5
US-09-010-877-2
```

```
; Sequence 2, Application US/09010877B
; Patent No. 644445
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Nikolich, Mikeljon
; APPLICANT: Hoover, David L.
; APPLICANT: Warren, Richard L.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Hadfield, Ted L.
; APPLICANT: Boyle, Stephen M.
; APPLICANT: McQuiston, John R.
; APPLICANT: Schurig, Gerhardt G.
; APPLICANT: Nannalwar Sriranganathan
; TITLE OF INVENTION: Live Vaccines Against Brucellosis
; FILE REFERENCE: Army-124
; CURRENT APPLICATION NUMBER: US/09/010,877B
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: No. 6444445e
; EARLIER FILING DATE: No. 6444445e
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PC-IBM compatible
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Brucella abortus
; US-09-010-877-2

Query Match      4.8%; Score 100.5; DB 4; Length 410;
Best Local Similarity 23.3%; Pred. No. 0.031;
Matches 59; Conservative 33; Mismatches 102; Indels 59; Gaps 13;

QY 69 DPDSYV-LSBSLSFYPLKIVIKTCGTTKLLTIPRILELAELSMLAAVKYSRGTFIF 127
Db 179 DAISYAGLPASKVYLAPMEF-----DPTFDRYRSVS-----KVKEPYFLW 219
QY 128 PGAPAPHRFSFSEVAALNRYFGLKSGGNAYVIGDPA----RPGQKWHVYATEYPEQM 184
Db 220 P-TNPNAKHAKAFQALDLYGKLGKIKTKIVGSSVRMDPSHRWQAKYEN---KAYV 275
QY 185 VNLEMCMGTGLDKK-----ACVFF-KTNADGNVTCAKEMTKLS-- 221
Db 276 KSVREIVAGLNLKSNVEFAGEVADKEYABELLASACFFHPTLADNGTFPAVAAVYMGCP 335
QY 222 GISEIPEMEICDFDF-PCGYSNNAIH-----GSASFTHIVTPEDGFSYASVYVGL--- 273
Db 336 TLSNDYFQKYEYISNRFEIPMQY-FNARSVKEMASALKQMEETPIDVGLLPSRETLSHSW 394
QY 274 DATALSYGDLVKR 286
Db 395 EAHASEYWDVIVR 407

RESULT 6
US-07-828-788A-14
; Sequence 14, Application US/07828788A
; Patent No. 5273746
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; Sequence 2, Application US/09010877B
; Patent No. 644445
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Nikolich, Mikeljon
; APPLICANT: Hoover, David L.
; APPLICANT: Warren, Richard L.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Hadfield, Ted L.
; APPLICANT: Boyle, Stephen M.
; APPLICANT: McQuiston, John R.
; APPLICANT: Schurig, Gerhardt G.
; APPLICANT: Nannalwar Sriranganathan
; TITLE OF INVENTION: Live Vaccines Against Brucellosis
; FILE REFERENCE: Army-124
; CURRENT APPLICATION NUMBER: US/09/010,877B
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: No. 6444445e
; EARLIER FILING DATE: No. 6444445e
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PC-IBM compatible
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Brucella abortus
; US-09-010-877-2

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,788A
; FILING DATE: 19920129
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA75
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B
; US-07-828-788A-14

Query Match      4.5%; Score 94; DB 1; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;

QY 35 VDPHGGLRALS-----RAQID-SVLDLARTIIVSELNKPDPDSYLVSESSL 80
Db 207 VDTNQGRLRGLRFLSDWIVNRRFRQLTISYLD-----IVAFFPNYDIRTYPIQTATQ 261
QY 81 FIVPLKIVIKTCGTTKLLTIPRILE-LABELSMLAAVKYSRGTFIFGAQPA---PH 135
Db 262 L-----TRVYLDLPFINENLSPAASYP-----TFSAESAIRSPH 298
QY 136 -----RSFSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPGQKWHVYATEYPE 181
Db 299 LVDFLNSFTIYTDLSARYAYWGHVNSFRGTGTTNLIRSPLYGREGNTERPVTITASPS 358
QY 182 QPMVNLEMCMGTGLDKKACVFFKTNADGNVTCAKEMTKLSGISEIPEMEICDFDFPC- 240
Db 359 VFIFRTLSYITGLDLSNPVAGIE-GVEFQNTISRSYRKSGPIDSFSELPQDASVSPAI 417
QY 241 GYSMNAIH-----GSASFTHI 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFWSWTH 446

RESULT 7
US-08-356-034-4
; Sequence 4, Application US/08356034
; Patent No. 5691308
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SalIWanchik & SalIWanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
```


Db 262 L-----TREVYLDLPFINENLSPAASYP-----TFSAESAIRSPH 298
Qy 136 ----RSFSEVAALNR--YFGG-----LKSGGNVAVIGDP--ARPOQKWHVFVATYPE 181
Db 299 LVDFLNSFTIYDLSARYAWGCHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
Qy 182 QPMVNLNEMCMTGDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDLSNPVAGIE-GVEFQNTISRSIYKSGPIDSPFSELPQDASVPAI 417
Qy 241 GYSNNAIH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFSWTH 446

RESULT 9

US-09-521-344-4
; Sequence 4, Application US/09521344
; Patent No. 6573240
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: Lepidopteran Bacillus thuringiensis Isolate Active Against
; TITLE OF INVENTION: Lepidopteran Pests, and Genes Encoding No. 6573240e1
; FILE REFERENCE: MA-43CDP2D2
; CURRENT APPLICATION NUMBER: US/09/521,344
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 08/933,891
; EARLIER FILING DATE: 1997-09-19
; EARLIER APPLICATION NUMBER: US 08/356,034
; EARLIER FILING DATE: 1994-12-14
; EARLIER APPLICATION NUMBER: US 08/210,110
; EARLIER FILING DATE: 1994-03-17
; EARLIER APPLICATION NUMBER: US 07/865,168
; EARLIER FILING DATE: 1992-04-09
; EARLIER APPLICATION NUMBER: US 07/451,261
; EARLIER FILING DATE: 1989-12-14
; EARLIER APPLICATION NUMBER: US 07/371,955
; EARLIER FILING DATE: 1989-06-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-521-344-4

Query Match 4.5%; Score 94; DB 4; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;
Qy 35 VDPHGRLRLS-----RAQID-SVLDLARCCTIVSELSNKNDFSDVLSSESL 80
Db 207 VDTYNOGLRLEGRFLSDWIVNRRQLTISVLD-----IVAFPNYDIRTYPIQTATQ 261
Qy 81 FIYPLKIVIKTCGTTKLLLTIPRILE-LABELSNPLAAVKYSGRTFFPGQAQA-----PH 135
Db 262 L-----TREVYLDLPFINENLSPAASYP-----TFSAESAIRSPH 298
Qy 136 ----RSFSEVAALNR--YFGG-----LKSGGNVAVIGDP--ARPOQKWHVFVATYPE 181
Db 299 LVDFLNSFTIYDLSARYAWGCHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
Qy 182 QPMVNLNEMCMTGDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDLSNPVAGIE-GVEFQNTISRSIYKSGPIDSPFSELPQDASVPAI 417
Qy 241 GYSNNAIH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFSWTH 446

RESULT 10
PCT-US92-11337-14
; Sequence 14, Application PC/TUS9211337
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE

RESULT 10

US-09-837-961A-4
; Sequence 4, Application US/09837961A
; Patent No. 6737273
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 6737273el Bacillus thuringiensis Isolate Active Against Lepid
; TITLE OF INVENTION: Pests, and Genes Encoding No. 6737273el Lepidopteran-Active Toxi
; FILE REFERENCE: MA-43CDP2D3
; CURRENT APPLICATION NUMBER: US/09/837,961A
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/521,344
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 08/933,891
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: US 08/356,034
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: US 08/210,110
; PRIOR FILING DATE: 1994-03-17
; PRIOR APPLICATION NUMBER: US 07/865,168
; PRIOR FILING DATE: 1992-04-09
; PRIOR APPLICATION NUMBER: US 07/451,261
; PRIOR FILING DATE: 1989-12-14
; PRIOR APPLICATION NUMBER: US 371,955
; PRIOR FILING DATE: 1989-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-837-961A-4

Query Match 4.5%; Score 94; DB 4; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;
Qy 35 VDPHGRLRLS-----RAQID-SVLDLARCCTIVSELSNKNDFSDVLSSESL 80
Db 207 VDTYNOGLRLEGRFLSDWIVNRRQLTISVLD-----IVAFPNYDIRTYPIQTATQ 261
Qy 81 FIYPLKIVIKTCGTTKLLLTIPRILE-LABELSNPLAAVKYSGRTFFPGQAQA-----PH 135
Db 262 L-----TREVYLDLPFINENLSPAASYP-----TFSAESAIRSPH 298
Qy 136 ----RSFSEVAALNR--YFGG-----LKSGGNVAVIGDP--ARPOQKWHVFVATYPE 181
Db 299 LVDFLNSFTIYDLSARYAWGCHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
Qy 182 QPMVNLNEMCMTGDKKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDLSNPVAGIE-GVEFQNTISRSIYKSGPIDSPFSELPQDASVPAI 417
Qy 241 GYSNNAIH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFSWTH 446

RESULT 11

PCT-US92-11337-14
; Sequence 14, Application PC/TUS9211337
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE

```
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11337
; FILING DATE: 19921231
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 97/828,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA75
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: P8811
; IMMEDIATE SOURCE:
; LIBRARY: LAMEDGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B
; PCT-US92-11337-14

Query Match 4.5%; Score 94; DB 5; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;

QY 35 VDPHGRGLRALS-----RAQID-SVLDLARTIVSELNKPDSYVLSSESL 80
Db 207 VDTYNQGLRLEGRFLSDMIVYNNRFRRLTISVLD-----IVAFFPNYDIRTYPIQTATQ 261
QY 81 FIYPLKIVIKTCGTTKLLLTIPRILE-LABELSNPLAAVKYSGRTFFPCAQA-----PH 135
Db 262 L-----TREYLDLPFINENLSPAASYP-----TFSAAESAIRSRPH 298
QY 136 -----RSFSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAYWGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
QY 182 QPMVNLEMCMTGLDKKACVFFKTNADGNTCAKEMTKLSGISEIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDNGNPVAGIE-GVEFQNTISRSYRKSGPIDSPSELPPQDASVSPAI 417
QY 241 GYSMNATH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFSWTH 446

RESULT 12
5188960-4
; Patent No. 5188960
; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
; LEPIDOPTERAN-ACTIVE TOXINS
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/451,261
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 371,955
; FILING DATE: 27-JUN-1989
; SEQ ID NO: 4:
; LENGTH: 1165
5188960-4

Query Match 4.5%; Score 94; DB 6; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;

QY 35 VDPHGRGLRALS-----RAQID-SVLDLARTIVSELNKPDSYVLSSESL 80
Db 207 VDTYNQGLRLEGRFLSDMIVYNNRFRRLTISVLD-----IVAFFPNYDIRTYPIQTATQ 261
QY 81 FIYPLKIVIKTCGTTKLLLTIPRILE-LABELSNPLAAVKYSGRTFFPCAQA-----PH 135
Db 262 L-----TREYLDLPFINENLSPAASYP-----TFSAAESAIRSRPH 298
QY 136 -----RSFSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAYWGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
QY 182 QPMVNLEMCMTGLDKKACVFFKTNADGNTCAKEMTKLSGISEIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDNGNPVAGIE-GVEFQNTISRSYRKSGPIDSPSELPPQDASVSPAI 417
QY 241 GYSMNATH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFSWTH 446

RESULT 13
5188960-4
; Patent No. 5188960
; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
; LEPIDOPTERAN-ACTIVE TOXINS
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/451,261
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 371,955
; FILING DATE: 27-JUN-1989
; SEQ ID NO: 4:
; LENGTH: 1165
5188960-4

Query Match 4.5%; Score 94; DB 6; Length 1165;
Best Local Similarity 23.4%; Pred. No. 1;
Matches 63; Conservative 30; Mismatches 100; Indels 76; Gaps 14;

QY 35 VDPHGRGLRALS-----RAQID-SVLDLARTIVSELNKPDSYVLSSESL 80
Db 207 VDTYNQGLRLEGRFLSDMIVYNNRFRRLTISVLD-----IVAFFPNYDIRTYPIQTATQ 261
QY 81 FIYPLKIVIKTCGTTKLLLTIPRILE-LABELSNPLAAVKYSGRTFFPCAQA-----PH 135
Db 262 L-----TREYLDLPFINENLSPAASYP-----TFSAAESAIRSRPH 298
QY 136 -----RSFSEVAALNR--YFGG-----LKSGGNAYVIGDP--ARPGQKWHVFVATEYPE 181
Db 299 LVDFLNSFTIYDLSARYAYWGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITASPS 358
QY 182 QPMVNLEMCMTGLDKKACVFFKTNADGNTCAKEMTKLSGISEIIPEMEICDFDFEPC- 240
Db 359 VPIFRTLSTYITGLDNGNPVAGIE-GVEFQNTISRSYRKSGPIDSPSELPPQDASVSPAI 417
QY 241 GYSMNATH-----GSAFSTIH 256
Db 418 GYSHRLCHATFLERISGPRIAGTVFSWTH 446

RESULT 12
5188960-4
; Patent No. 5188960
; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
; LEPIDOPTERAN-ACTIVE TOXINS
; NUMBER OF SEQUENCES: 8
```


QY 241 GYSNNAIH-----GSAFSTIH 256
 Db 418 GYSRLCHATFLERISGRIAGTWFVSWTH 446

RESULT 14

US-08-773-368-1
 ; Sequence 1, Application US/08773368
 ; Patent No. 5856130
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08773,368
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy RJ
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0186 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 270 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: 1599164
 ;
 US-08-773-368-1

Query Match 4.4%; Score 91.5; DB 2; Length 270;
 Best Local Similarity 23.2%; Pred. No. 0.16;
 Matches 63; Conservative 28; Mismatches 108; Indels 73; Gaps 16;
 QY 97 LLITIPRILELA-----EELSMPLAAVKYSGRTIFPGAPAPHRSPSEVAAL 145
 Db 8 LMLLLPLLVLAVTTGPGVGTALDEEKKLMVELHNLVYRAQ-VSPASDMLHMRWDELAALF 66
 QY 146 NRYFGGL-----KSGGNAYVIGDPA-----PGQKWHVFYATEYPPQPMVNLE--M 189
 Db 67 AKAYARQXRKHNGRGRGENLFAITDEGMDVPLAMEWH-----HEREHYNLSAAT 119
 QY 190 CMTGLDKKAC-----VFFKTNADGNNTCAKEM-TKLSGISIIPMEICDF----- 235
 Db 120 CSPG-----QMGCHYTQVWAKTERIG---CGSHFCEKLGQVEETNIELLVNTEPPGNVK 172
 QY 236 -----DFEPCGYSMNAIH--GSAFSTIHTVPDGG--FSYASYEVNGLDATALSYGDLVK 285
 Db 173 GKRPYQEGTFCSPGSGYHCKNSLCEPIG-SPEDAQDPLVLTAPSPFRATEAS-----DS 227
 QY 286 RVLRCFGPSEFSAVTIFGGRGHAGTWGKALG 317

Db 228 RKGAEKDPKPSVYVSGLNSGPHG--VWGPXLG 257

RESULT 15

US-09-199-887-1
 ; Sequence 1, Application US/09199887
 ; Patent No. 6071874
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09199,887
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/773,368
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy RJ
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0186 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 270 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: 1599164
 ;
 US-09-199-887-1

Query Match 4.4%; Score 91.5; DB 3; Length 270;
 Best Local Similarity 23.2%; Pred. No. 0.16;
 Matches 63; Conservative 28; Mismatches 108; Indels 73; Gaps 16;
 QY 97 LLITIPRILELA-----EELSMPLAAVKYSGRTIFPGAPAPHRSPSEVAAL 145
 Db 8 LMLLLPLLVLAVTTGPGVGTALDEEKKLMVELHNLVYRAQ-VSPASDMLHMRWDELAALF 66
 QY 146 NRYFGGL-----KSGGNAYVIGDPA-----PGQKWHVFYATEYPPQPMVNLE--M 189
 Db 67 AKAYARQXRKHNGRGRGENLFAITDEGMDVPLAMEWH-----HEREHYNLSAAT 119
 QY 190 CMTGLDKKAC-----VFFKTNADGNNTCAKEM-TKLSGISIIPMEICDF----- 235
 Db 120 CSPG-----QMGCHYTQVWAKTERIG---CGSHFCEKLGQVEETNIELLVNTEPPGNVK 172
 QY 236 -----DFEPCGYSMNAIH--GSAFSTIHTVPDGG--FSYASYEVNGLDATALSYGDLVK 285
 Db 173 GKRPYQEGTFCSPGSGYHCKNSLCEPIG-SPEDAQDPLVLTAPSPFRATEAS-----DS 227
 QY 286 RVLRCFGPSEFSAVTIFGGRGHAGTWGKALG 317

Db 228 RKMGAEGDPKPSVVSLNSGFGH--VMGPXLG 257

Search completed: May 11, 2005, 22:53:54
Job time : 28.4605 secs

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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:36:02 ; Search time 102.062 Seconds
(without alignments)

1515.788 Million cell updates/sec

Title: US-10-732-923-408

Perfect score: 2097

Sequence: 1 MAVLSAADSPVSAIGPEGY.....LLCWEEDAMBEKAGVLDE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2097	100.0	400	8 ADM48040	Adm48040 Polypepti
2	1687.5	80.5	366	8 ADM48039	Adm48039 Polypepti
3	1019	48.6	237	7 ABM73860	Abm73860 DNA clone
4	933.5	44.5	360	2 AAR75006	Aar75006 Tomato S-
5	933	44.5	363	5 AAU79674	Aau79674 Cucurbita
6	933	44.5	363	7 ABG75228	Abg75228 Plant wit
7	933	44.5	363	8 ADP90956	Adp90956 Fig leaf g
8	933	44.5	363	8 ADR38366	Adr38366 Fig leaf
9	881	42.0	366	3 AAG28816	Agag28816 Arabidops
10	806.5	38.5	309	7 ABM73938	Abm73938 DNA clone
11	478.5	22.8	155	7 ABM74096	Abm74096 DNA clone
12	466	22.2	368	8 ADN22644	Adn22644 Bacterial
13	466	22.2	368	8 ADN22643	Adn22643 Bacterial
14	437.5	20.9	369	8 ADN19900	Adn19900 Bacterial
15	424	20.2	348	3 AAB56589	Aab56589 Human pro
16	421.5	20.1	348	4 ABG05997	Abg05997 Novel hum
17	420	20.0	334	5 AAU84313	Aau84313 Protein A
18	420	20.0	334	7 ADE60574	Ad60574 Human Pro
19	420	20.0	334	7 ADD48325	Add48325 Human Pro
20	420	20.0	334	7 ADE60570	Ad60570 Human Pro
21	420	20.0	334	7 ADD48321	Add48321 Human Pro
22	420	20.0	334	8 ADN03708	Adn03708 Antipori
23	420	20.0	334	8 ADQ88208	Adq88208 Human 912
24	419	20.0	333	7 ADE60568	Ad60568 Rat Prote
25	419	20.0	333	7 ADD48323	Add48323 Rat Prote

ALIGNMENTS

RESULT 1

ADM48040
ID ADM48040 standard; protein; 400 AA.

XX AC ADM48040;

XX XX
DT 03-JUN-2004 (first entry)

DE Polypeptide sequence #90 useful in producing transgenic plants.

XX Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
KW osmotic stress; sugar transport; cell cycle pathway; plant height;
KW carbohydrate transport; crop productivity; plant growth;
KW stress resistance; disease resistance; insect resistance; heat tolerance;
KW nitrogen assimilation; water stress tolerance;
KW photosynthetic carbon fixation; virus resistance; gene therapy.
XX Zea mays.

XX XX
PN US2003233670-A1.

XX XX
PD 18-DEC-2003.

XX XX
PF 04-DEC-2002; 2002US-00310154.

XX XX
PR 04-DEC-2001; 2001US-0337358P.

XX XX
PA (EDGE/) EDGERTON M D.

XX XX
PA (CHOM/) CHOMET P S.

XX XX
PA (LACC/) LACCETTI L B.

XX XX
PI Edgerton MD, Chomet PS, Laccetti LB;

XX XX
DR WPI; 2004-061374/06.

XX XX
DR N-PSDB; ADM47672.

XX XX
PT New polynucleotide, useful for manipulating plant protein quality,
PT improving plant growth, yield and crop productivity or grain composition
PT or producing plants with improved properties.

XX XX
PS Claim 8; SEQ ID NO 458; 144pp; English.

XX XX
CC The present invention relates to polynucleotide sequences, and the
CC proteins they encode. The sequences are isolated from a variety of
CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
CC polynucleotide and polypeptide sequences of the invention are useful in
CC the production of transgenic plants that have improved properties. Also

CC disclosed are methods of producing fertile transgenic plants, preferably
 CC maize, with desired phenotypes. The polynucleotide and polypeptide
 CC sequences are useful for improving plants by providing protection against
 CC osmotic stress, improving altering sugar transport and/or metabolism,
 CC modifying the cell cycle pathway, reducing plant height, modifying
 CC carbohydrate transport, improving crop productivity, improving plant
 CC growth and stress resistance, improving disease resistance, improving
 CC insect resistance, improving cold or heat tolerance, improving nitrogen
 CC assimilation, improving stalk strength, improving water stress tolerance,
 CC improving photosynthetic carbon fixation, improving biotic and abiotic
 CC stress resistance, improving resistance to oxidative stress, providing
 CC increased vigour, reducing senescence, and conferring virus resistance.
 CC The present sequence represents a polypeptide sequence of the invention.
 CC Note: The sequence data for this patent is not provided in the printed
 CC specification but is obtained in electronic format from the USPTO website
 CC at seqdata.uspto.gov.

XX SQ Sequence 400 AA;

Query Match 100.0%; Score 2097; DB 8; Length 400;
 Best Local Similarity 100.0%; Pred. No. 4.1e-206;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAVLSAADASPVSAIGPEGYKLEITFSAPVDPVDPHGLRLSRAQIDSVLDLACT 60
 DB 1 MAVLSAADASPVSAIGPEGYKLEITFSAPVDPVDPHGLRLSRAQIDSVLDLACT 60
 QY 61 IVSELSNKDFSDVSVLSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKY 120
 DB 61 IVSELSNKDFSDVSVLSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKY 120
 QY 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGLKSGGNAYVIGDPAFGQKHVYATEYP 180
 DB 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGLKSGGNAYVIGDPAFGQKHVYATEYP 180
 QY 181 EQMVNLEMCWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
 DB 181 EQMVNLEMCWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
 QY 241 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGLDATALSYGDLVKVRLRCFGSFSVAV 300
 DB 241 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGLDATALSYGDLVKVRLRCFGSFSVAV 300
 QY 301 TIFGGRGHAGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAEADAVATSPKSVFHC 360
 DB 301 TIFGGRGHAGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAEADAVATSPKSVFHC 360
 QY 361 DGENVESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE 400
 DB 361 DGENVESAPPPMKDYKLANLLCWEEADAMEEKAGVLDE 400

RESULT 2

ADMA48039

ID ADMA48039 standard; protein; 366 AA.

XX AC ADMA48039;

XX DT 03-JUN-2004 (first entry)

XX DE Polypeptide sequence #89 useful in producing transgenic plants.

XX KW Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;

XX KW osmotic stress; sugar transport; cell cycle pathway; plant height;

XX KW carbohydrate transport; crop productivity; plant growth;

XX KW stress resistance; disease resistance; insect resistance; heat tolerance;

XX KW nitrogen assimilation; water stress tolerance;

XX KW photosynthetic carbon fixation; virus resistance; gene therapy.

XX OS Zea mays.

XX XX US2003233670-A1.

XX PN

XX XX

PD 18-DEC-2003.
 XX 04-DEC-2002; 2002US-00310154.
 XX 04-DEC-2001; 2001US-0337358P.
 XX (EDGE/) EDGERTON M D.
 PA (CHOM/) CHOMET P S.
 XX (LACC/) LACCETTI L B.
 XX Edgerton MD, Chomet PS, Laccetti LB;
 XX WPI; 2004-061374/06.
 DR N-PSDB; ADMA7671.
 XX New polynucleotide, useful for manipulating plant protein quality,
 PT improving plant growth, yield and crop productivity or grain composition
 PT or producing plants with improved properties.
 XX Claim 8; SEQ ID NO 457; 144pp; English.

XX The present invention relates to polynucleotide sequences, and the
 CC proteins they encode. The sequences are isolated from a variety of
 CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
 CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
 CC polynucleotide and polypeptide sequences of the invention are useful in
 CC the production of transgenic plants that have improved properties. Also
 CC disclosed are methods of producing fertile transgenic plants, preferably
 CC maize, with desired phenotypes. The polynucleotide and polypeptide
 CC sequences are useful for improving plants by providing protection against
 CC osmotic stress, improving altering sugar transport and/or metabolism,
 CC modifying the cell cycle pathway, reducing plant height, modifying
 CC carbohydrate transport, improving crop productivity, improving plant
 CC growth and stress resistance, improving cold or heat tolerance, improving
 CC insect resistance, improving stalk strength, improving water stress tolerance,
 CC assimilation, improving carbon fixation, improving biotic and abiotic
 CC stress resistance, improving resistance to oxidative stress, providing
 CC increased vigour, reducing senescence, and conferring virus resistance.
 CC The present sequence represents a polypeptide sequence of the invention.
 CC Note: The sequence data for this patent is not provided in the printed
 CC specification but is obtained in electronic format from the USPTO website
 CC at seqdata.uspto.gov.

XX SQ Sequence 366 AA;

Query Match 80.5%; Score 1687.5; DB 8; Length 366;
 Best Local Similarity 85.0%; Pred. No. 4.4e-164;
 Matches 328; Conservative 7; Mismatches 20; Indels 31; Gaps 2;
 QY 1 MAVLSAADASPVSAIGPEGYKLEITFSAPVDPVDPHGLRLSRAQIDSVLDLACT 60
 DB 1 MAVLSAADASPVSAIGPEGYKLEITFSAPVDPVDPHGLRLSRAQIDSVLDLACT 60
 QY 61 IVSELSNKDFSDVSVLSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKY 120
 DB 59 -----KIVIKTCGTTKLLLTIPRILELAELSMPAAVKY 93
 QY 121 SRGTFFPGAQAPHRFSFSEVAALNRYFGLKSGGNAYVIGDPAFGQKHVYATEYP 180
 DB 94 SRGTFFPGAQAPHRFSFSEVAALNRYFGLKSGGNAYVIGDPAFGQKHVYATEYP 153
 QY 181 EQMVNLEMCWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
 DB 154 EQMVNLEMCWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 213
 QY 241 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGLDATALSYGDLVKVRLRCFGSFSVAV 300
 DB 214 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGLDATALSYGDLVKVRLRCFGSFSVAV 273
 QY 301 TIFGGRGHAGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAEADAVATSPKSVFHC 360
 DB 274 TIFGGRGHAGTWGKALGAEVYDCNNMVEQELPGGGLLVYQSFCAEADAVATSPKSVLRCF 333

Db	241	EGAAVSTHITPDGFTYASFESGVDPKTNELGPLVERVLACPEPAERSIAL-----	293
Qy	308	HAGTWGKAL-----GAEVDCNNWQELPGGGLLYQSFCAEDAVATSPKSVFHC	361
Db	294	HADVATKLLSHVCSVDVKYSLAEWSPEFGKGSIVYQKF--TRTPCYCSPKSVLKG--	349
Qy	362	GENVESAPPPMKDYKLANLLCWEEEDAMEEKAG	396
Db	350	-----CWKE-----EKEG	358
RESULT 5			
AAU79674			
ID	AAU79674	standard; protein; 363 AA.	
XX	AC	AAU79674;	
XX	DT	15-JUL-2002 (first entry)	
XX	DE	Cucurbita ficifolia S-adenosylmethionine decarboxylase (SAMDC).	
XX	KW	Plant; polyamine metabolism-related enzyme; environmental stress;	
KW	KW	vegetable; fruit; flower; food; agriculture; horticulture;	
KW	KW	temperature stress; drought; improved growth; SAMDC;	
KW	KW	S-adenosylmethionine decarboxylase; enzyme.	
XX	OS	Cucurbita ficifolia.	
XX	XX	WO200223974-A1.	
XX	PD	28-MAR-2002.	
XX	XX	31-AUG-2001; 2001WO-JP007521.	
XX	PR	20-SEP-2000; 2000JP-00285423.	
XX	PR	08-FEB-2001; 2001JP-00032627.	
XX	PA	(TOYO-) TOYOBO RES CENT CO LTD.	
XX	PI	Kasukabe Y, Ihara I, Tachibana S;	
XX	DR	WPI; 2002-329978/36.	
XX	DR	N-PSDB; ABK48732.	
XX	PT	Plant for selecting new breeds of e.g. vegetables, fruits and flowers for	
PT	PT	food and decoration, comprises improved tolerance to environmental	
PT	PT	stresses transferred with a plant-originated polyamine metabolism-	
PT	PT	relating enzyme gene.	
XX	PS	Disclosure; Page 85-88; 108pp; Japanese.	
XX	CC	The present invention relates to the isolation of a plant derived	
CC	CC	polyamine metabolism-related enzyme gene. Also described is a plant	
CC	CC	having improved tolerance to environmental stresses that can stably	
CC	CC	sustain an exogenous polyamine metabolism-related enzyme gene by	
CC	CC	regulation of a promoter functioning in such plant, as compared to plants	
CC	CC	free from the exogenous gene, or its descendants. The plant is useful in	
CC	CC	selecting new breeds of e.g. vegetables, fruits and flowers for food and	
CC	CC	decoration, particularly applicable in agriculture and horticulture. The	
CC	CC	transgenic plants have improved tolerance to various environmental	
CC	CC	stresses e.g. temperature and drought, and also have excellent growth.	
CC	CC	The present sequence represents Cucurbita ficifolia S-adenosylmethionine	
CC	CC	decarboxylase (SAMDC)	
XX	SQ	Sequence 363 AA;	
Query Match		44.58; Score 933; DB 5; Length 363;	
Best Local Similarity		50.98; Pred. No. 1.5e-86;	
Matches		201; Conservative 53; Mismatches 95; Indels 46; Gaps 9;	
Qy	11	PVSAIGFEGYKRLTFTSPVFDVPHGRGLRALSQAQIDSLDLARCTIVSELNKF	70
Db	4	PTSAIGFEGYKRLVSPFPGIFADPRGNGRLALSQAQIDSLDLARCTIVSELNKF	63

Qy	71	DSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKYSGTFFPGA	130
Db	64	DSYVLSSESLFVYPYPIKTCGTTKLLSIPALIKLADSLNLSVSVYTRGSFIFPGA	123
Qy	131	QPAPHRFSFSEVAALNRYFGGLKSGGNVYVIGDPAKPGQKWHFYAT-----EYEQPMVN	186
Db	124	QSPFHRFSFSEVAALNRYFGGLKSGGNVYVIGDPAKPGQKWHFYAT-----EYEQPMVN	182
Qy	187	LEMCMTGLDKKACVFFKTNADONTTCAKEMTKLSGISEIIPMEICDFDFPEPCGYSMNA	246
Db	183	LEMCMTGLDKKACVFFKTNADONTTCAKEMTKLSGISEIIPMEICDFDFPEPCGYSMNA	238
Qy	247	IHGSAPSTHVTPEDEGSYASVEVMGLDATALSYGDLVKVLCRCFSGSESVAVTIIGGR	306
Db	239	IEGDAESTHVTPEDEGSYASVEVMGLDATALSYGDLVKVLCRCFSGSESVAVTIIGGR	292
Qy	307	GHAGTWGK-----ALGAEVYDCNNWVEQELPGGGLLYQSFCAEDAVATSPKSVFHC	360
Db	293	-HSDVVGEDLKDLLCLDLKGYEGEKSCMLGENGSVIYQSFKNRGD-YASSPRLSIL---	347
Qy	361	DGENVESAPPPMKDYKLANLLCW-BEEDAMEEK	394
Db	348	-----MK-----CCWREDEADEEVEK	363
RESULT 6			
ABG75228			
ID	ABG75228	standard; protein; 363 AA.	
XX	AC	ABG75228;	
XX	DT	12-FEB-2004 (first entry)	
XX	DE	Plant with improved organogenesis related protein SEQ ID NO: 4.	
XX	KW	Organogenesis; polyamine metabolism-associated gene; transgenic;	
KW	KW	drug production; biodegradable plastic; enzyme production;	
KW	KW	vaccine production; promoter; plant; callus.	
XX	OS	Cucurbita ficifolia.	
XX	XX	WO2003084314-A1.	
XX	PD	16-OCT-2003.	
XX	PF	08-APR-2003; 2003WO-JP004427.	
XX	PR	08-APR-2002; 2002JP-00105583.	
XX	PA	(TOYO-) TOYOBO RES CENT CO LTD.	
XX	PI	Kasukabe Y, Ihara I, Tachibana S, Matsui K, Mizutani M;	
XX	DR	WPI; 2003-833547/77.	
XX	DR	N-PSDB; ACP04931.	
XX	PT	Construction of plants with improved organogenesis of e.g. stem, leaf,	
PT	PT	flower, fruit or seed for retaining plant-originated polyamine metabolism	
PT	PT	-associated gene, applicable in producing useful substances including	
PT	PT	drugs.	
XX	XX	Claim 7; Page 70-72; Opp; Japanese.	
XX	PS	The present invention relates to plants and their offspring which stably	
CC	CC	retain 1 or more nucleic acid sequences for regulating polyamine dose	
CC	CC	under the control of a promoter functionally in the plant and have at	
CC	CC	least an improved organogenesis as compared with plants without such	
CC	CC	nucleic acid sequences. The constructed plants are applicable in	
CC	CC	producing useful substances including drugs, biodegradable plastics,	
CC	CC	vaccines and enzymes. Such method is particularly applicable in	
CC	CC	agriculture and horticulture. The present sequence is a protein shown in	
CC	CC	the exemplification of the invention	

```

XX SQ Sequence 363 AA;
Query Match 44.5%; Score 933; DB 7; Length 363;
Best Local Similarity 50.9%; Pred. No. 1.5e-86;
Matches 201; Conservative 53; Mismatches 95; Indels 46; Gaps 9;

QY 11 PVSAGFEGYKRLTFTSEAPVFDPHGRGLRALSRQAIDSVDLACTIVSELSNKF 70
DB 4 PVSAGFEGYKRLTFTSEAPVFDPHGRGLRALSRQAIDSVDLACTIVSELSNKF 63
QY 71 DSVLSESSLFYPLKIVTKTCTGTTKLLIPRILELAELSMPAAVKYSGRTFPPGA 130
DB 64 DSVLSESSLFYPLKIVTKTCTGTTKLLIPRILELAELSMPAAVKYSGRTFPPGA 123
QY 131 QPAPHRFSFEVAALNRYFGLKSGNAYVIGDPARPGQKWHVFYAT---EYPEQPMVN 186
DB 124 QSPFHRFSFEVAALNRYFGLKSGNAYVIGDPARPGQKWHVFYAT---EYPEQPMVN 182
QY 187 LEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMNA 246
DB 183 LEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMNA 238
QY 247 IHGSAFTIHTVTPEDGFSYASVEVMGLDATALSYGLDLVKVLCFCGSPSESVAVTIFGGR 306
DB 239 IEGDAESTIHTVTPEDGFSYASVEVMGLDATALSYGLDLVKVLCFCGSPSESVAVTIFGGR 292
QY 307 GHAGTGWK-----ALGAEVYDCNNVVEQELPGGLLVYQSCAAEDAVATSPKSVPHCF 360
DB 293 -HSDVVGEDLKDLLCLDLKGYEGEKSCEMLGENGSVIYQSFKNRGD-YASSPRSL--- 347
QY 361 DGENVESAPPMKKDYKLANLLCW-BEEDAMBEK 394
DB 348 -----MK-----CCWREDEADEVEK 363

RESULT 7
ADP90956
ID ADP90956 standard; protein; 363 AA.
AC ADP90956;
XX
XX
XX
XX 23-SEP-2004 (first entry)
DE Figleaf gourd S-adenosylmethionine decarboxylase (SAMDC) 1814 protein.
XX plant; environmental stress resistance; polyamine promoter; fat; oil;
XX cellulose; hydrocarbon; pigment; enzyme production; natural rubber;
XX pharmaceutical; figleaf gourd; S-adenosylmethionine decarboxylase;
XX SAMDC 1814; enzyme; EC 4.1.1.50.
XX
XX Cucurbita ficifolia.
XX
XX JP2004180588-A.
XX
XX 02-JUL-2004.
XX
XX 03-DEC-2002; 2002JP-00351750.
XX
XX 03-DEC-2002; 2002JP-00351750.
XX
XX (TOYO-) TOYOBO SOGO KENKYUSHO KK.
XX
XX WPI; 2004-472277/45.
XX
XX N-PSDB; ADP90956.
XX
XX Novel plant exhibiting improved environmental stress resistance and
XX having nucleic acid controlling amount of polyamines, useful for
XX obtaining substances such as fat and oil, cellulose, and natural rubber.
XX
XX Example 1; SEQ ID NO 4; 69pp; Japanese.
XX
XX The invention relates to a novel plant, or its offspring, exhibiting

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CC improved environmental stress resistance and having a nucleic acid which
CC controls the amount of polyamines under the control of a promoter that
CC functions in the plant, compared with the plant which does not possess
CC the nucleotide and where the nucleotide is maintained stably within the
CC plant. The polynucleotide of the invention may be useful for obtaining
CC substances such as fat and oil, cellulose, hydrocarbon, pigment, enzymes,
CC natural rubber and pharmaceutical compounds. The plant has improved
CC oxidative stress, herbicide, salt, osmotic pressure, water or low
CC temperature resistance. The current sequence is that of the figleaf gourd
CC S-adenosylmethionine decarboxylase (SAMDC) 1814 protein of the invention.
XX
XX Sequence 363 AA;
Query Match 44.5%; Score 933; DB 8; Length 363;
Best Local Similarity 50.9%; Pred. No. 1.5e-86;
Matches 201; Conservative 53; Mismatches 95; Indels 46; Gaps 9;

QY 11 PVSAGFEGYKRLTFTSEAPVFDPHGRGLRALSRQAIDSVDLACTIVSELSNKF 70
DB 4 PVSAGFEGYKRLTFTSEAPVFDPHGRGLRALSRQAIDSVDLACTIVSELSNKF 63
QY 71 DSVLSESSLFYPLKIVTKTCTGTTKLLIPRILELAELSMPAAVKYSGRTFPPGA 130
DB 64 DSVLSESSLFYPLKIVTKTCTGTTKLLIPRILELAELSMPAAVKYSGRTFPPGA 123
QY 131 QPAPHRFSFEVAALNRYFGLKSGNAYVIGDPARPGQKWHVFYAT---EYPEQPMVN 186
DB 124 QSPFHRFSFEVAALNRYFGLKSGNAYVIGDPARPGQKWHVFYAT---EYPEQPMVN 182
QY 187 LEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMNA 246
DB 183 LEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFDFPCGYSMNA 238
QY 247 IHGSAFTIHTVTPEDGFSYASVEVMGLDATALSYGLDLVKVLCFCGSPSESVAVTIFGGR 306
DB 239 IEGDAESTIHTVTPEDGFSYASVEVMGLDATALSYGLDLVKVLCFCGSPSESVAVTIFGGR 292
QY 307 GHAGTGWK-----ALGAEVYDCNNVVEQELPGGLLVYQSCAAEDAVATSPKSVPHCF 360
DB 293 -HSDVVGEDLKDLLCLDLKGYEGEKSCEMLGENGSVIYQSFKNRGD-YASSPRSL--- 347
QY 361 DGENVESAPPMKKDYKLANLLCW-BEEDAMBEK 394
DB 348 -----MK-----CCWREDEADEVEK 363

RESULT 8
ADP90956
ID ADP90956 standard; protein; 363 AA.
AC ADP90956;
XX
XX
XX 18-NOV-2004 (first entry)
XX
XX Fig leaf gourd S-adenosylmethionine decarboxylase (SAMDC) protein SeqID 4.
XX transgenic; plant; productivity; polyamine metabolism; fig leaf gourd;
XX S-adenosylmethionine decarboxylase; SAMDC; enzyme.
XX
XX Cucurbita ficifolia.
XX
XX JP2004242510-A.
XX
XX 02-SEP-2004.
XX
XX 10-FEB-2003; 2003JP-00032606.
XX
XX 10-FEB-2003; 2003JP-00032606.
XX
XX (TOYO-) TOYOBO SOGO KENKYUSHO KK.
XX
XX WPI; 2004-608540/59.
XX
XX N-PSDB; ADP90956.

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```
XX Enhanced plant e.g. sweet potato, has transgenic plant with better
PT productivity and character regardless of cultivation environment compared
PT to plant without nucleic acid.
XX
XX Example 1; SEQ ID NO 4; 56pp; Japanese.
XX
CC This invention relates to a novel transgenic plant with improved
CC productivity. Specifically, it refers to transforming a plant, for
CC example a sweet potato, rose, sunflower, tobacco or shiitake mushroom,
CC with a nucleic acid molecule. This DNA molecule encoding an enzyme that
CC modulates polyamine metabolism such that the plant is stably maintained.
CC The present invention describes a method to improve the appearance of the
CC plant, for example the stalk, bud, flower petal or fruit, and thus
CC improve the commercial value of the plant. This polypeptide sequence is
CC the fig leaf gourd S-adenosylmethionine decarboxylase (SAMDC) protein,
CC encoded by a polyamine metabolism related gene of the invention.
XX
SQ Sequence 363 AA;
Query Match 44.5%; Score 933; DB 8; Length 363;
Best Local Similarity 50.9%; Pred. No. 1.5e-86;
Matches 201; Conservative 53; Mismatches 95; Indels 46; Gaps 9;
QY 11 PVSAIGFEGYEKLEITFFSEAPVVDPHGRGLRALSRQAIDSVLDLARCTIVSELNKNDF 70
DB 4 PTAIGFEGYEKLEIVSFFPFGIFADPRGMLRALSKAQLDEILTAECTIVDSLSNDYL 63
QY 71 DSVLSESSLIYPLKIVIKTCGTKLLLTPIRILEAEELSMPLAAVKYSRGTFIPPGA 130
DB 64 DSVLSESSLIYVYPIKTCGTKLLLTPIRILEAEELSMPLAAVKYSRGTFIPPGA 123
QY 131 QPAPHSFSEVAALNRYFGLKSGGNAYVIGPARPGQKWHVFYAT----EYEQPMVN 186
DB 124 QSPFHSFSEVAALNRYFGLKSGGNAYVIGPARPGQKWHVFYAT----EYEQPMVN 182
QY 187 LEWMTGLDKKACVPKTTNADGNTTCAKMTKLSGISEIIPMEICDFPFCGYSMNA 246
DB 183 LEWMTGLDKKASVPKTTNADGNTTCAKMTKLSGISEIIPMEICDFPFCGYSMNA 238
QY 247 IHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRLRCFGSPSEFSAVTIFGGR 306
DB 239 IEGDAESTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRLRCFGSPSEFSAVTIFGGR 292
QY 307 CHAGTWCK-----ALCAEYVDCNWNVEQELPGGLLVYQSFCAEADAVATSPKSVPHCF 360
DB 293 -HSDVVGEDLKDLLCLDKGEGEKSCMLGNGSVIYQSFKNRGD-YASSPRSL--- 347
QY 361 DGENVESAPPMKKDYKLANLLCW-EEADAMEEK 394
DB 348 -----MK-----CCWREDADEVEEK 363
RESULT 9
AAG28816
ID AAG28816 standard; protein; 366 AA.
XX
AC AAG28816;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 34176.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; Genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX
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PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 25-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129045P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
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PR 11-MAY-1999; 99US-0134256P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
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PR 09-JUL-1999; 99US-0142920P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 42.0%; Score 881; DB 3; Length 366;
Best Local Similarity 50.7%; Pred. No. 3 4e-81;
Matches 185; Conservative 49; Mismatches 95; Indels 36; Gaps 8;

QY 12 VSAIGFEGYEKRLKLEITFSEAPVDPHGRGLRALSRAQIDSVLDLACTIVSELNKPFD 71
Db 3 LSAIGFEGYEKRLKLEITFSEAPVDPHGRGLRALSRAQIDSVLDLACTIVSELNKPFD 62
QY 72 SYVLSESSLIPIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKYSGTFFPQAQ 131
Db 63 SYVLSESSFPVYPIYIKTCGTTKLLLTIPRILELAELSMPAAVKYSGTFFPQAQ 122
QY 132 PAPHRSFSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVFYATYEPQPMVN---L 187
Db 123 PPHRSFSEVSVLDGHTQLGLNSVAYLMGNDDET-KKWHVYAAQAQSSNCNNVYTL 181
QY 188 EMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISSEIPEMEICDFPFCGYSNNAI 247
Db 182 EMCMTGLDKREKAAVFKDEADKTGS---MTDNGIRKILPKSEICDFEFCGYSNNSI 237
QY 248 HGSASFSTIHVTPEDGFSYASYEVMGLDATALSYGDLVKVLRFCGFSERSVATIFGGRG 307
Db 238 EGDASTIHVTPEDGFSYASFEAVGYDFNTLDLSQLVTRVLSCFEPKQFSVAV----- 290
QY 308 HAGTWGKALGAEV-----YDCNNMVEQEL-PGGGLLVYQSF-----CAEADAVATSPK 354
Db 291 HSSVGANSYKPEITVDLEDYGCRTFESLGESGTVMTQTFEKLKYCG-----SPR 343
QY 355 SVFPHC 359
Db 344 STLKC 348

RESULT 10
ABM73938
ID ABM73938 standard; protein; 309 AA.

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XX AC ABW73938;
XX DT 17-OCT-2003 (first entry)
XX DE DNA clone originating in barley containing SNP sequence #348.
XX KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
XX OS Hordeum vulgare.
XX PN WO2003057877-A1.
XX PD 17-JUL-2003.
XX PF 16-DEC-2002; 2002WO-IB005403.
XX PR 20-DEC-2001; 2001JP-00387059.
XX PR 20-DEC-2001; 2001JP-00387131.
XX PR 20-DEC-2001; 2001JP-00403299.
XX PR 20-DEC-2001; 2001JP-00403300.
XX PR 27-SEP-2002; 2002JP-00327515.
XX PA (UYNI-) UNIV JAPAN OKAYAMA.
XX PI Sato K, Takeda K, Kohara Y;
XX DR WPI; 2003-587127/55.
XX SS Single nucleotide polymorphism sites in barley varieties and DNA
XX PT sequences containing them for analysis and identification of barley
XX PT varieties and production of barley transformants with desired
XX PT characteristics.
XX PS Disclosure; SEQ ID XX; 284pp; Japanese.
XX CC The present invention relates to oligonucleotide clones originating in
XX CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
XX CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
XX CC varieties, identification of particular varieties and genotype-phenotype
XX CC analysis, isolation of specific genes and creation of new varieties by
XX CC transformation of barley varieties with them and production of new barley
XX CC varieties with desired properties. The present sequence represents an
XX CC oligonucleotide clone sequence featured in the specification. The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published-pct-sequences
XX SQ Sequence 309 AA;
XX
Query Match 38.5%; Score 806.5; DB 7; Length 309;
Best Local Similarity 64.8%; Pred. No. 1.2e-73;
Matches 171; Conservative 13; Mismatches 47; Indels 33; Gaps 4;

QY 68 KDFDSYVLSSSLFIYPLKIVIKTCGTTKLLITIPRILEAEELSMPLAAVKYSGTFF 127
DB 31 RFDSDYVLSSSLFIYSQKIVIKTCGTTMLLLIPRILEAEELCMPLAAVKYSGRMFIF 90
QY 128 PGAQAPHRFSFEVVALNRYFGLKSGGNAYVIGDPAPQKQWVFYATEYPEQPMVNL 187
DB 91 PGAQAPHRFSFEVDVNLRYFGLHKSNGNAYVIGDPAKFGQKWHIYATEYPEQPMVTL 150
QY 188 EMCWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFE----- 238
DB 151 EMCWTGLDKKASVFFKTSADGHVCAKEMTKLSGISNIIPEMEVCDFDFEALRLHLHERH 210
QY 239 -----PCGYSNNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGLVKVRLC 290
DB 211 QRCLLHHPCDPRRTASATAMRSRAWTPPP-WSTATSSRGSGSALQ-----SS 260
QY 291 FGPSEFSVAVTIFGGRGHAGTWGK 314
DB 261 LWRSPSSVAA-----GHAATWGO 278

RESULT 11
ABM74096
ID ABM74096 standard; protein; 155 AA.
XX AC ABM74096;
XX DT 17-OCT-2003 (first entry)
XX DE DNA clone originating in barley containing SNP sequence #506.
XX KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
XX OS Hordeum vulgare.
XX PN WO2003057877-A1.
XX PD 17-JUL-2003.
XX PF 16-DEC-2002; 2002WO-IB005403.
XX PR 20-DEC-2001; 2001JP-00387059.
XX PR 20-DEC-2001; 2001JP-00387131.
XX PR 20-DEC-2001; 2001JP-00403299.
XX PR 20-DEC-2001; 2001JP-00403300.
XX PR 27-SEP-2002; 2002JP-00327515.
XX PA (UYNI-) UNIV JAPAN OKAYAMA.
XX PI Sato K, Takeda K, Kohara Y;
XX DR WPI; 2003-587127/55.
XX SS Single nucleotide polymorphism sites in barley varieties and DNA
XX PT sequences containing them for analysis and identification of barley
XX PT varieties and production of barley transformants with desired
XX PT characteristics.
XX PS Disclosure; SEQ ID XX; 284pp; Japanese.
XX CC The present invention relates to oligonucleotide clones originating in
XX CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
XX CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
XX CC varieties, identification of particular varieties and genotype-phenotype
XX CC analysis, isolation of specific genes and creation of new varieties by
XX CC transformation of barley varieties with them and production of new barley
XX CC varieties with desired properties. The present sequence represents an
XX CC oligonucleotide clone sequence featured in the specification. The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published-pct-sequences
XX SQ Sequence 155 AA;
XX
Query Match 22.8%; Score 478.5; DB 7; Length 155;
Best Local Similarity 64.2%; Pred. No. 2.1e-40;
Matches 97; Conservative 15; Mismatches 30; Indels 9; Gaps 2;

QY 244 MNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGLVKVRLCFCGPSEFSVATIF 303
DB 1 MNAIHGSAFSTIHTVTPEDGFSYGYEVMGLDPASMAVGLVKVRLSGFSGSEFSVATIF 60
QY 304 GGRGHAGTWGKALGAEYVDCNNVVEQLPGGGLLVYQSFCAEADAVATSPKSFHCFDGE 363
DB 61 GCFSLAGTWGERLNVGYDSTNNVQELPGGGLLVYQSFCAEADAVATSPKSFHCFDGE 120
QY 364 NVESAPPPMKKQYKLANLLCWESEADAMEEK 394
DB 121 NLQAS-----KVDAFLCWED--DAAQEK 142

RESULT 12

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ADN22644	ADN22644 standard; protein; 368 AA.	QY	6	AADASPVA-----IGPEGYEKRLITFSEAPVDPHGRGLRALSRAQIDSVLDLARCTI	61
XX		DB	10	AVOTHPKAPDEBYFEGAELKLELWFCSS---TQNETSLRIIPREIDAMLDIARCKI	66
XX		QY	62	VSELSNKFDSYVLSSESSIFLYPLKIVIKTCGTTKLLLTIPRILELAELUS--MPLAAVK	119
XX		DB	67	LHSHKNEISDYVLSSESSIFISDNVILKTCGTTLLAALFVIMQLAGAYAGLDQVQSVY	126
XX		QY	120	YSRGTTFPGAPAPHRSEFSEVAALNRYFGLKSGNAVIGDPPARPGOKWVHF---YA	176
XX		DB	127	YSKNFLRDLQPSLHKNFDAVEYLDSPF---VDGHAYCLGSLKQ--DRWLYTHFRE	180
XX		QY	177	TEYP--EQPMVNLEMWMTGLDKKACVFFKXTNA-DGNTTCAKEMTKLSGISEIPE-MEI	232
XX		DB	181	VEFPAHKQPDHTLEILMSDLDEVLHKFTKDYAVDGNDCPMR-----AGIDKIIPAGADV	235
XX		QY	233	CDPDPFCGYSMNAINHSA--FSTIHVTPEDGFSYASYEVMGLDATALSYGDLV----	284
XX		DB	236	HDELFPDPCGYSMNAYMNDTDQVATHVTPEKAFSFAFE-----TNQDLVCLYSQT	286
XX		QY	285	KRVLCRFGPSEFSVAVTIFGGRGHAGTWGKALCAEVYDCNNMVEQELPG	333
XX		DB	287	RKVLQCFRENK--ILMTVFA--NDISEKGDAAQQQLWD-----RELPG	325
XX		DE	RESULT 13		
XX		ADN22643	ADN22643 standard; protein; 368 AA.		
XX		AC	ADN22643;		
XX		DT	02-DEC-2004 (first entry)		
XX		DE	Bacterial polypeptide #5296.		
XX		XX	Recombinant DNA construct; transformed plant; improved plant property;		
XX		KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;		
XX		KW	pathogen tolerance; pest tolerance; plant disease resistance;		
XX		KW	cell cycle pathway modification; plant growth regulator;		
XX		KW	homologous recombination; seed oil yield; protein yield; carbohydrate;		
XX		KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;		
XX		XX	bacterial polypeptide.		
XX		OS	Bacteria.		
XX		PN	US2003233675-A1.		
XX		XX	18-DEC-2003.		
XX		PF	20-FEB-2003; 2003US-00369493.		
XX		PR	21-FEB-2002; 2002US-0360039P.		
XX		PA	(CAOY/) CAO Y.		
XX		PA	(HINK/) HINKLE G J.		
XX		PA	(SLAT/) SLATER S C.		
XX		PA	(CHEN/) CHEN X.		
XX		PA	(GOLD/) GOLDMAN B S.		
XX		XX	Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;		
XX		XX	WPI; 2004-061375/06.		
XX		PT	New recombinant DNA construct comprising a promoter positioned to provide		
XX		PT	for expression of a polynucleotide encoding a polypeptide from a		
XX		PT	microbial source, useful for producing plants with improved properties.		
XX		PS	Claim 1; SEQ ID NO 5297; 122pp; English.		
XX		CC	The invention relates to a recombinant DNA construct comprising a		
XX		CC	promoter functional in a plant cell, where the promoter is positioned to		
XX		CC	provide for expression of a polynucleotide encoding a polypeptide from a		
XX		CC	microbial source. The invention also relates to a transformed plant		
XX		CC	comprising the recombinant DNA construct and a method of producing a		
XX		CC	transformed plant having an improved property. The plant is a crop plant		
XX		CC	such as maize or soybean. The method of producing a transformed plant		
XX		CC	having an improved property comprises transforming a plant with the		
XX		CC	recombinant DNA construct and growing the transformed plant, where the		
XX		CC	polynucleotide or polypeptide is useful for improving plant properties.		
XX		CC	The recombinant DNA construct is useful for producing plants with		
XX		CC	improved plant properties, e.g. improved cold, heat or drought tolerance,		
XX		CC	tolerance to herbicides, extreme osmotic conditions, pathogens or pests,		
XX		CC	increased resistance to plant disease, better growth rate by modification		
XX		CC	of the cell cycle pathway with plant growth regulators, increased rate of		
XX		CC	homologous recombination, modified seed oil or protein yield and/or		
XX		CC	content, improved yield by modification of carbohydrate, nitrogen or		
XX		CC	phosphorus use and/or uptake, by modification of photosynthesis or by		
XX		CC	providing improved plant growth and development under at least one stress		
XX		CC	condition. Improved lignin production or improved galactomannan		
XX		CC	production. This sequence represents a bacterial polypeptide used in the		
XX		CC	scope of the invention. Note: The sequence data for this patent did not		
XX		CC	form part of the printed specification but was obtained in electronic		
XX		CC	format from USPTO at seqdata.uspto.gov/sequence.html.		
XX		XX	Sequence 368 AA;		
XX		XX	Query Match		
XX		XX	Best Local Similarity		
XX		XX	Matches 127; Conservative		
XX		XX	22.2%; Score 466; DB 8; Length 368;		
XX		XX	36.4%; Pred. No. 1.5e-38;		
XX		XX	Matches 127; Conservative		
XX		XX	62; Mismatches 106; Indels 54; Gaps 16;		

Claim 1; SEQ ID NO 5296; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 368 AA;

Query Match 22.2%; Score 466; DB 8; Length 368;
Best Local Similarity 36.4%; Pred. No. 1.5e-38;
Matches 127; Conservative 62; Mismatches 106; Indels 54; Gaps 16;
QY 6 AADASPVA---IGFEGYKRLITFSEAPVDPHGRGLRALSAQIDSVLDLACTI 61
DB 10 AVQTHPKADPEEYFEGAEKLELWPCSS---TQNETSLRIIPREIDAMLDIARCKI 66
QY 62 VSLSNKPDPYSVLSSESLFIYPLKIVIKTCGTTKLLITPRILELAELS--MPLAAVK 119
DB 67 LSHKNEISIDSVLSSESLFISDNVILKTCGTRLLAALPVMQLAGAYAGLDQVQSVY 126
QY 120 YSRGTTFPCAQAPAPHRFSFEVAALNRYFGLKSGGNAYVIGDPAAPGQKHVF---YA 176
DB 127 YSRKFLRDLQSLHKNFADAEVYLDSPF---VDGHAYCLSLKQ--DRWLYTFHRE 180
QY 177 TEYP--EQPMVNLMCGMTGLDKKACVFFKTNADGNNTCAKEMTKLSGISEIPE-MEI 232
DB 181 VEPFAHKQPDHTLEILMSDLDEEVHLKFTKDYAVDGNDCPMR-----AGIDKIIPAGADV 235
QY 233 CDFDFPCGYSMAIHGSA--FSTHTPDPGFSYASYEVMGLDATALSYGDLV----- 284
DB 236 HDELFDPGYSMAYNMNDTDQYATIHVTPEKAFSPASFE-----TNQDLVCLYSQT 286
QY 285 KRVLCFGPSEFSVAVTFGGRGHAGTWGKALGAEVYDCNNVVEQLPG 333
DB 287 RKVLQCFRPNK--ILMTVFA--NDISEKGDAAQQQLWD-----RELPG 325

RESULT 14

ADN19900

ID ADN19900 standard; protein; 369 AA.

XX AC ADN19900;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #2553.

XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX Bacteria.

PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 2553; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or by
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 369 AA;

Query Match 20.9%; Score 437.5; DB 8; Length 369;

Best Local Similarity 30.7%; Pred. No. 1.3e-35;

Matches 117; Conservative 77; Mismatches 118; Indels 69; Gaps 18;

QY 3 VLSAADASPVAISGFEYKRLITFSEAPV---DPHGRGLRALSAQIDSVLDLA 57

DB 6 VVDQNSEEFNTSSFEKLELWFS-APITNLSAGEKANGLKAVSRNDMDMLAQ 64

QY 58 RTIVSELNKPDPYSVLSSESLFIYPLKIVIKTCGTTKLLITPRILELAELS--PL 115

DB 65 QCKVSVNSEEIDAYLLSESNFVFAHKILKTCGTTLLASLPRLLEIATSSVGPDRPL 124

QY 116 AAVKYSRGTFIPGAQAPAPHRFSFEVAALNRYFGLKSGGNAYVIGDPAAPQK--WHV 173

DB 125 -RIFYRKNFPLYERQALPHTSWEEVRYLQFPF---PSGCSYVVG---PTNKHWHL 175

QY 174 P--YATEY-----PEQPMVNLMCGMTGLDKKACVF-----KT 205

DB 176 FSLADYDLSLSDLPEDF--TLEVLMTDMSPSRLQFYAPSLDVVRSGDDYVREKN 233

QY 206 NADGNTTCAKEMTKLSGISEIPEME---ICD--FDFEPCGYSMAIHGSAFSTIHTVTPD 261

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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:38:57 ; Search time 86.9416 Seconds
(without alignments)
2167.492 Million cell updates/sec

Title: US-10-732-923-407

Perfect score: 1914

Sequence: 1 MAVLSAAGAPPASAIQFEGY.....NLVCLREDAIERKGVLDLDE 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1726	90.2	400	1	DCAM_MAIZE	O24575 zea mays (m
2	1538	80.4	398	1	DCAM_ORYZA	O24215 oryza sativ
3	1538	80.4	398	2	O7X783	O7X783 oryza sativ
4	1472.5	76.9	393	1	DCAM_HORCH	O42829 hordeum chi
5	1460	76.3	392	2	O9ZFR1	Q9ZP11 triticum ae
6	1458	76.2	395	2	O6K9B8	O6K9B8 oryza sativ
7	1458	76.2	395	2	O9SC67	O9SC67 oryza sativ
8	1244	65.0	392	2	O6F4N6	O6F4N6 oryza sativ
9	1187.5	62.0	370	2	O84LA2	O84LA2 narcissus p
10	1160	60.6	369	2	O944U3	Q944U3 dendrobium
11	1134.5	59.3	339	2	O7F8M2	O7F8M2 oryza sativ
12	858	44.8	358	2	O7XZQ9	O7XZQ9 vitis vinif
13	854.5	44.6	357	1	DCAM_CATRO	O42679 catharanthu
14	851	44.5	353	1	DCAM_VICFA	Q9M448 vicia faba
15	841	43.9	363	1	DCAM_SPIOL	P46255 spinacia ol
16	836	43.7	362	1	DCAM_IPONI	Q96471 ipomoea nil
17	834.5	43.6	361	1	DCAM_NICSY	O80402 nicotiana s
18	834.5	43.6	361	1	DCAM_TOBAC	O04009 nicotiana t
19	834	43.6	353	1	DCAM_PEA	O43820 pisum sativ
20	833.5	43.5	349	2	O9LSU6	Q9LSU6 arabidopsis
21	833.5	43.5	358	2	O852S9	Q852S9 malus domes
22	832.5	43.5	374	2	O852S8	Q852S8 malus domes
23	830	43.4	362	1	DCAM_DATST	Q96555 datura stra
24	830	43.4	362	1	DCAM_IPOBA	Q9M6X1 ipomoea bat
25	826.5	43.2	354	2	O8W3Y2	O8W3Y2 phaseolus l
26	825.5	43.1	381	1	DCAL_DIACA	Q39676 dianthus ca
27	824.5	43.1	377	1	DCA2_DIACA	Q39677 dianthus ca
28	821.5	42.9	361	1	O8LKK7	O8LKK7 x citrofor
29	812.5	42.5	360	1	DCAM_SOLTU	Q04694 solanum tub
30	809	42.3	355	2	O8S3F8	O8S3F8 glycine max
31	798.5	41.7	361	2	O6RUQ3	O6RUQ3 daucus caro

32	792.5	41.4	361	1	DCAM_DAUCA	Q9axe3 daucus caro
33	771.5	40.3	366	1	DCAL_ARATH	Q96286 arabidopsis
34	769.5	40.2	366	2	O6QJ69	O6QJ69 brassica ju
35	766.5	40.0	366	2	O94Q05	Q94005 arabidopsis
36	763.5	39.9	361	1	DCAM_HELAN	O65354 helianthus
37	763	39.9	367	1	DCAJ_BRAJU	Q98d88 brassica ju
38	757	39.6	362	1	DCA2_ARATH	Q98719 arabidopsis
39	753	39.3	369	2	O6SZS4	O6SZS4 brassica ju
40	751	39.2	369	1	DCA2_BRAJU	O49972 brassica ju
41	718.5	37.5	279	2	O76KV7	O76KV7 pisum sativ
42	706.5	36.9	368	1	DCAL_BRAJU	O42613 brassica ju
43	668.5	34.9	309	2	O6KC47	O6KC47 prunus pers
44	609.5	31.8	169	2	O9SC65	O9SC65 oryza sativ
45	574.5	30.0	228	2	O8VX33	O8VX33 vitis vinif

ALIGNMENTS

```

RESULT 1
DCAM_MAIZE          STANDARD;          PRT;    400 AA.
AC  O24575;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE  (SambC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
DE  adenosylmethionine decarboxylase beta chain].
GN  Name=SAMDC;
OS  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  PACC4D clade; Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxID=4577;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Michael A.J.;
RL  Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC  -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
CC  adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
CC  -I- COFACTOR: Pyruvoyl group (By similarity).
CC  -I- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC  aminopropyl moiety required for spermidine and spermine
CC  biosynthesis from putrescine.
CC  -I- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  use by non-profit institutions as long as its content is in no way
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CC  or send an email to license@isb-sib.ch).
-----
CC  EMBL: Y07767; CAA69075.1; -.
CC  PIR: T03947; T03947.
CC  HSP: P17707; IJEN.
CC  InterPro: IPR001985; SAM decarbox.
CC  Pfam: PF01536; SAM decarbox; 1.
CC  ProDom: PD002379; SAM decarbox; 1.
CC  TIGRfam: TIGR00535; SAM DCcase; 1.
CC  PROSITE: PS01336; ADOMETDC; 1.
CC  Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymoegen.
CHAIN 1 77 S-adenosylmethionine decarboxylase beta
      CHAIN 78 400 chain (By similarity).
      CHAIN 77 78 S-adenosylmethionine decarboxylase alpha
      SITE 77 78 chain (By similarity).
      MOD_RES 78 78 Cleavage (nonhydrolytic) (By similarity).
      ACT_SITE 18 18 Pyruvic acid (Ser) (By similarity).
      ACT_SITE 21 21 By similarity.
      ACT_SITE 92 92 By similarity.

```


OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12447439; DOI=10.1038/nature01183;
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Wang L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lu G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Shao X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 DR EMBL; AL606594; CAE01625.2; -;
 DR EMBL; AL606627; CAD41242.2; -;
 DR HSSP; P17707; 117B.
 DR Gramene; Q7X183; -;
 DR Gramene; Q7X183; -;
 DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spermine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 SQ SEQUENCE 398 AA; 43283 MW; BC24F359962F8655 CRC64;
 Query Match 80.4%; Score 1538; DB 2; Length 398;
 Best Local Similarity 77.0%; Pred. No. 3.2e-120;
 Matches 308; Conservative 18; Mismatches 40; Indels 34; Gaps 5;
 QY 1 MAVLSAAGAPASAIPEGVEKLEITFSEAPVDPHGSLRALSRQSDSVLDLAR-- 58
 DB 1 MGVLAAADPPVSAIPEGVEKLEITFSEAPVDPHGSLRALSRQSDSVLDLARCT 60
 QY 59 -----KIVIKTCGTTKLLTIPRIELAEBSMPLAAVKY 93
 DB 61 IVSELNSKDPDSYVLSSESLFIYSKDIKIVIKTCGTTKLLTIPRIELAEBSMPLAAVKY 120
 QY 94 SRTGTFPGAQAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDAPRGQKWHIYYATEVP 153
 DB 121 SRGWFIFPSAQAAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDAPRGQKWHIYYATQHP 180
 QY 154 EQPMVLEMCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 213
 DB 181 EQPMVLEMCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPC 240
 QY 214 GYSMNAIHGSAFSTIHTVPDGFSGSYAEVWGLDATALSYGDLVXRVLCFGFSEPSVAV 273
 DB 241 GYSMNAIHGSAFSTIHTVPDGFSGSYAEVWGLDATALSYGDLVXRVLCFGFSEPSVAV 300
 QY 274 TIFGGRGQAGTWKELGAENAYDCNNMVEQBELPGGILLIYQSCAAED--AVASSPKSVLR 331
 DB 301 TIFGGRGQAGTWKELNADAYKCNMVEQBELPGGILLIYQSCAAED--AVASSPKSVLR 360
 QY 332 CFDEG---NAAPAKCKLANVLCLEXDAIEBKGVLD 368
 DB 361 CFEAENMVNPAP-VKEGKGLNLLPWGE-DALENDGVFDE 398
 RESULT 4
 DCAM_HORCH
 ID DCAM_HORCH STANDARD; PRT; 393 AA.
 AC Q42829;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
 DE (Samdc) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
 DE adenosylmethionine decarboxylase beta chain].
 GN Name=SAMDC;
 OS Hordeum chilense (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=15565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=96270379; PubMed=8639739;
 RA Dresselhaus T., Barcelo P., Hagel C., Loefer H., Humbeck K.;
 RT "Isolation and characterization of a Tritordeum cDNA encoding S-
 RT adenosylmethionine decarboxylase that is circadian-clock-regulated.";
 RL Plant Mol. Biol. 30:1021-1033(1996).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S)-deoxy-5-
 CC adenosyl (3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -1- COFACTOR: Pyruvoyl group.
 CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
 CC aminopropyl moiety required for spermidine and spermine
 CC biosynthesis from putrescine.
 CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; X83881; CAAS8762.1; -;
 DR PIR; S69191; S69191.
 DR HSSP; P17707; 1JEN.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
 FT CHAIN 1..70 S-adenosylmethionine decarboxylase beta
 FT chain (By similarity).
 FT CHAIN 71..393 S-adenosylmethionine decarboxylase alpha
 FT chain (By similarity).
 FT SITE 70..71 Cleavage (nonhydrolytic) (By similarity).
 FT MOD_RES 71..71 Pyruvic acid (Ser) (By similarity).
 FT ACT_SITE 11..11 By similarity.
 FT ACT_SITE 14..14 By similarity.
 FT ACT_SITE 85..85 By similarity.
 SQ SEQUENCE 393 AA; 42895 MW; 6CD1AA94792AF6CB CRC64;
 Query Match 76.9%; Score 1472.5; DB 1; Length 393;
 Best Local Similarity 74.6%; Pred. No. 9.5e-115;
 Matches 290; Conservative 25; Mismatches 43; Indels 31; Gaps 4;
 QY 9 APPASAIPEGVEKLEITFSEAPVDPHGSLRALSRQSDSVLDLAR----- 58
 DB 2 AAPVSAIPEGVEKLEITFSEASIFADPHGRGLRALSRQSDSVLDLARCTTVSELSNK 61
 QY 59 -----KIVIKTCGTTKLLTIPRIELAEBSMPLAAVKYSGRTFIPP 101
 DB 62 DFDVYVLSSESLFIYSKDIKIVIKTCGTTKLLTIPRIELAEBSMPLAAVKYSGRTFIPP 121
 QY 102 GAQPAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDAPRGQKWHIYYATEYPPQPMVNL 161
 DB 122 GAQPAPHRFSFSEVAVLNRYFGLKSGGNAYVIGDAPRGQKWHIYYATEYPPQPMVNL 181
 QY 162 MCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPCGYSMNAIH 221
 DB 182 MCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDPEPCGYSMNAIH 241

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QY 222 GSASFTHVTPEDGFSYASVEVWGLDATALSYGDLVKRVLCGPGSPSEFSAVAVTFGRGQ 281
Db 242 GSASFTHVTPEDGFSYASVEVWGLDATALSYGDLVKRVLCGPGSPSEFSAVAVTFGRGH 301
QY 282 AGTWKGLGAEAYDCNNMVQEQLPGGGILLIYQSFCAEDAV--ASSPKSVLRCFDG-ENA 338
Db 302 AATWKKLDAAEDYDCNNVVEQLPCGGVLLIYQSFANEEELAVSAGSPRSVFHCFENVESG 361
QY 339 APFAKCKLANLVCL-EXDAIEBKDGLV 366
Db 362 HPLVKEGKLANLLAWRAEBSLEGTGAL 390

RESULT 5
Q92PJ1 ID Q92PJ1 PRELIMINARY; PRT; 392 AA.
AC Q92PJ1
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S-adenosylmethionine decarboxylase.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Z.Y., Chen S.Y.
RT "Isolation and characterization of a salt and drought-inducible gene
RT for S-adenosylmethionine decarboxylase from wheat (Triticum aestivum
RT L.).";
RL J. Plant Physiol. 156:386-393 (2000).
DR EMBL; AF117660; AAD17232.1; -.
DR HSP; P17707; IJEN.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:permethidine biosynthesis; IEA.
DR GO; GO:0006597; P:permethidine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRfam; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETC; 1.
SQ SEQUENCE 392 AA; 42854 MW; C761765631C2E91F CRC64;

Query Match 76.3%; Score 1460; DB 2; Length 392;
Best Local Similarity 74.3%; Pred. No. 1.1e-113;
Matches 287; Conservative 25; Mismatches 41; Indels 32; Gaps 4;

QY 9 APPASIGFEGYKRLKLEITFSEAPVFDPHGSLRALSRQIDSVLDLAR----- 58
Db 2 AAPTASIGFEGYKRLKLEITFSEAPVFDPHGSLRALSRQIDSVLDLARCTIVSELSTK 61
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSMPLAAVKYGRGFIP 101
Db 62 DPOSYVLSSESLIYQKIVIKTCGTTKLLTIPRILELAELSMPLAAVKYGRGFIP 121
QY 102 GAQPAPHRSPSEAVNLNRYFGGLKSGGNAYVIGDAARPGQKWHIYATPEYPPQVWVLE 161
Db 122 GAQAPHRSPSEAVNLNRYFGHLKSGGNAYVIGDAARPGQKWHIYATPEYPPQVWVLE 181
QY 162 MCMTGLDTKASVFFKTNADGNNTCAKEMTKLSGISSEIIPEMEICDFDFPCGYSMAIH 221
Db 182 MCMTGLDKKASVFFKTNADGNNTCAKEMTKLSGISSEIIPEMEICDFDFPCGYSMAIH 241
QY 222 GSASFTHVTPEDGFSYASVEVWGLDATALSYGDLVKRVLCGPGSPSEFSAVAVTFGRGQ 281
Db 242 GSASFTHVTPEDGFSYASVEVWGLDATALSYGDLVKRVLCGPGSPSEFSAVAVTFGRGH 301
QY 282 AGTWKGLGAEAYDCNNMVQEQLPGGGILLIYQSFCAEDAV--ASSPKSVLRCFDG--N 337
Db 302 AATWKKLDAAEDYDCNNVVEQLPCGGVLLIYQSFANEEELAVSAGSPRSVFHCFEAESVH 361

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QY 338 AAPFAKCKLANLVCL-EXDAIEB 361
Db 362 SHPLVKEGKLANLLAWRAEBSLEE 386

RESULT 6
Q6K9B8 ID Q6K9B8 PRELIMINARY; PRT; 395 AA.
AC Q6K9B8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE S-adenosylmethionine decarboxylase 2.
GN Name=OJ1476_F05.33; Synonyms=OJ1004_A05.7;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004063; BAD19232.1; -.
DR EMBL; AP005286; BAD19677.1; -.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:permethidine biosynthesis; IEA.
DR GO; GO:0006597; P:permethidine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRfam; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETC; 1.
SQ SEQUENCE 395 AA; 43152 MW; 49C9BC56F20FE540 CRC64;

Query Match 76.2%; Score 1458; DB 2; Length 395;
Best Local Similarity 73.0%; Pred. No. 1.6e-113;
Matches 286; Conservative 25; Mismatches 47; Indels 34; Gaps 3;

QY 1 MAVLSAAGAPPASIGFEGYKRLKLEITFSEAPVFDPHGSLRALSRQIDSVLDLAR-- 58
Db 1 MAVLSVADSPPVSAIGFEGYKRLKLEITFSEAPVFDPHGSLRALSRQIDSVLDLARCT 60
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSMPLAAVKY 93
Db 61 IVSELNEVFDVSVLSESLFVVPYKIVIKTCGTTKLLTIPRILELAELSMPLAAVKY 120
QY 94 SRGTFFPQAQAPHRSPSEAVNLNRYFGGLKSGGNAYVIGDAARPGQKWHIYATPEY 153
Db 121 SRGTFFPQAQAPHRSPSEAVNLNRYFGGLKSGGNAYVIGDAARPGQKWHIYATQHP 180
QY 154 EQPMVNLWCMTGLDTKASVFFKTNADGNNTCAKEMTKLSGISSEIIPEMEICDFDFPC 213
Db 181 EQPMVNLWCMTGLDKKASVFFKTNADGNNTCAKEMTKLSGISSEIIPEMEICDFDFPC 240
QY 214 GYSMNAIHGSAFSTIHTVTPEDGFSYASVEVWGLDATALSYGDLVKRVLCGPGSPSEVAV 273
Db 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASVEVWGLDATALSYGDLVKRVLCGPGSPSEVAV 300
QY 274 TIFGGRGQAGTWKGLGAEAYDCNNMVQEQLPGGGILLIYQSFCAEDAVASSPKSVLRCF 333
Db 301 TIFGGRHAGTWKGLDVGRAYSNNVVEQLPSGGLLIYQSFATAETATGSPRSVLHCF 360
QY 334 DGENAAPFAKCKLANLVCL-EXDAIEBKD 364
Db 361 ADENTE-----KAGKMEALYWDDEAVEIDG 386

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RESULT 7
ID Q9SC67 PRELIMINARY; PRT; 395 AA.
AC Q9SC67;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE S-adenosylmethionine decarboxylase 2 (BC 4.1.1.50).
DE S-adenosylmethionine decarboxylase 2 (BC 4.1.1.50).
GN Name:adomctc2;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2106509; PubMed=11139406; DOI=10.1042/0264-6021:3530403;
RA Franceschetti M., Hanfrey C., Scaramagli S., Torrigiani P., Begni N.,
RA Michael A.J.;
RT "Characterization of moncot and dicot plant S-adenosyl-methionine
RT decarboxylase gene families including identification in the mRNA of a
RT highly conserved pair of upstream overlapping open reading frames.";
RL Biochem. J. 353:403-409(2001).
DR EMBL; AJ251899; CAB64600.1; -.
DR HSSP; P17707; IJEN.
DR Gramene; Q9SC67; -.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Lyase.
SQ SEQUENCE 395 AA; 43152 MW; 49C9BC56F20F540 CRC64;

Query Match 76.2%; Score 1458; DB 2; Length 395;
Best Local Similarity 73.0%; Pred. No. 1.6e-113;
Matches 286; Conservative 25; Mismatches 47; Indels 34; Gaps 3;

QY 1 MAVLSAAGAPPASAIPEGYKLEITFSAPVFDPHGSLRALSRQSDSVLDLAR-- 58
DB 1 MAVLSVADSPVSAIPEGYKLEITFSAPVFDPHGSLRALSRQSDSVLDLARCT 60
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSPLAAVKY 93
DB 61 IVSELSNEVDSYVLSSESLFVYPYKIVIKTCGTTKLLLAIPRILELAELSPLAAVKY 120
QY 94 SRTGTFPPGAQAPAPHSFSEVAVLNRYFGGLKSGGNAYVIGDAPRGQKWHIYYATEYP 153
DB 121 SRTGTFPPGAQAPAPHSFSEVAVLNRYFGGLKSGGNAYVIGDAPRGQKWHIYYATQHP 180
QY 154 EQPMVNLWCMTGLDTKKASVFFKTNADGNNTTCAKEMTKLSGISEIIPENIEICDFDFEPC 213
DB 181 EQPVTLEMCMTGLDCKAASVFFKTSADGHTTAKEMTKLSGSDIIPENIEICDFDFEPC 240
QY 214 GYSNNAIHGSAFSTIHTVPDGFYSASYEVWGLDATALSYGDLVKRVLCFGSFSVAV 273
DB 241 GYSNNAIHGSAFSTIHTVPDGFYSASYEVWGLDATALSYGDLVKRVLCFGSFSVAV 300
QY 274 TIFGGGQAGTWCKELGAEAYDCNNMVEQLPGGGLIYQSFCAEDAVASSPKSVLRCP 333
DB 301 TIFGGRNHAGTWCKELGAEAYDCNNMVEQLPGGGLIYQSFCAEDAVASSPKSVLRCP 360
QY 334 DGENAAPFAKDCCKLANLVCLLE-EXDAIEEKDG 364
DB 361 ADENTE-----KAGKMEALYWDVDAVEEDIG 386

RESULT 8
Q6F4N6
ID Q6F4N6 PRELIMINARY; PRT; 392 AA.
AC Q6F4N6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE S-adenosylmethionine decarboxylase.
DE S-adenosylmethionine decarboxylase.
GN Name=SAMDCL1; Synonym=P0418B08.27-1;
OS Oryza sativa (Japanese cultivar group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15215597;
RA Yamaguchi T., Nakayama K., Hayashi T., Yazaki J., Kishimoto N.,
RA Kikuchi S., Koike S.;
RT "cDNA Microarray Analysis of Rice Anther Genes under Chilling Stress
RT at the Microsporogenesis Stage Revealed Two Genes with DNA Transposon
RT Castaway in the 5'-Flanking Region.";
RL Biosci. Biotechnol. Biochem. 68:1315-1323(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
RT clone:P0418B08.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB122089; BAD26704.1; -.
DR EMBL; AF005420; BAD33432.1; -.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 392 AA; 42717 MW; 0DF1F61522C38FE3 CRC64;

Query Match 65.0%; Score 1244; DB 2; Length 392;
Best Local Similarity 62.8%; Pred. No. 1.3e-95;
Matches 244; Conservative 48; Mismatches 68; Indels 30; Gaps 3;

QY 1 MAVLSAAGAPPASAIPEGYKLEITFSAPVFDPHGSLRALSRQSDSVLDLAR-- 58
DB 3 MSLADSWGSPASPIGFEYKLEITLSDAPVFDPCGRLALSRQSDSVLDLARCT 62
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSPLAAVKY 93
DB 63 IVSHLSNKHFDSDYVLSSESLFVYPYKIVIKTCGTTKLLLAIPRILELAELSPLAAVKY 122
QY 94 SRTGTFPPGAQAPAPHSFSEVAVLNRYFGGLKSGGNAYVIGDAPRGQKWHIYYATEYP 153
DB 123 SRGMFIPGAQSPHRSFSEVAVLNRYFGGLKSGGNAYVIGDAPRGQKWHIYYATEEP 182
QY 154 EQPMVNLWCMTGLDTKKASVFFKTNADGNNTTCAKEMTKLSGISEIIPENIEICDFDFEPC 213
DB 183 EQPVTLEMCMTGLDCKAASVFFKTSADGHTTAKEMTKLSGISEIIPENIEICDFDFEPC 242
QY 214 GYSNNAIHGSAFSTIHTVPDGFYSASYEVWGLDATALSYGDLVKRVLCFGSFSVAV 273
DB 243 GYSNNGIYGPVASTIHTVPDGFYSASYEVWGLDATALSYGDLVKRVLCFGSFSVAV 302
QY 274 TIFGGGQAGTWCKELGAEAYDCNNMVEQLPGGGLIYQSFCAEDAVASSPKSVLRCP 333
DB 303 TIFGGHGFSAKSAAGAEVDSVDCMDLVLEQLPGGGLIYQSFCAEDAVASSPKSVLRCP 361
QY 334 DGENAAPFAKDCCKLANLVCLLE-EXDAIEEKDG 363
DB 362 NSDGAEWAKSKEMS--VCWEGEKAAXKDD 389

RESULT 9

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Q84LA2
ID Q84LA2 PRELIMINARY; PRT; 370 AA.
AC Q84LA2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S-adenosylmethionine decarboxylase.
GN Name=Samdc;
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=4-day old flower tepals;
RA Gookin T.E., Cabauatan E.V., Hunter D.A., Reid M.S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232672; AAC043186.1; -.
DR HBL; P17707; IJEN.
DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spERMINE biosynthesis; IEA.
DR GO; GO:0006597; P:spERMINE biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 370 AA; 40680 MW; 36F619BA4806F70F CRC64;

Query Match 62.0%; Score 1187.5; DB 2; Length 370;
Best Local Similarity 60.7%; Pred. No. 6.5e-91;
Matches 229; Conservative 48; Mismatches 57; Indels 43; Gaps 3;

Qy 13 SAIGFEGYKRLTTFSEAPVFDVPHGSGRLALRSQIDSVLDLAR----- 58
Db 7 SPIGFEGYKRLTTFSEAPVFDVPHGSGRLALRSQIDSVLDLARCTIVHLNKKDFDS 66
Qy 59 -----KIVIKTCGTTKLLTIPRILELAELSMPLAAYKYSRGTFIPGAQP 105
Db 67 YVLSSESLFYPCMKILKTCGTTLLLSIPVILDLAELSLSVTAVKYSRGTFIPGAQP 126
Qy 106 AHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPGQKHYYATYEPPEPMVNLKMT 165
Db 127 TPRHNSPEEVALDHFGNLAGSNAYVIGDPSPNRHHYYATQPELPTVLEKMT 186
Qy 166 GLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDFPCGYSMNAIHGSF 225
Db 187 GLDSEKASIFNPGNANNAQSKMTKLSGISNIIPMEICDFDFPCGYSMNAICSAH 246
Qy 226 STIHVTPEDGFSYASVEVWGLDATALSYGLVKRVLCGFPSPFSVAVTIFGGRGQAGTW 285
Db 247 STIHVTPEDGSSYASVEAMGNFAELDFGGLVERVLECFGPAFDSVAVTIFGGRGQAGSW 306
Qy 286 GKELGAEAYDCNNMVDELPGGGLIYQSCAAEDAVASSPKSVLRFCFDGENAAPPKDC 345
Db 307 GREVDYSGFRCVLDVLELQAGGLIYQSFAGVGRM-GSPRSTLHCWDGEE----- 357
Qy 346 KLANVLCLEEXDAIEEK 362
Db 358 -----IEEKAEDKK 367

RESULT 10
Q944U3
ID Q944U3 PRELIMINARY; PRT; 369 AA.
AC Q944U3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S-adenosyl-L-methionine decarboxylase.
GN Name=Samdc;
OS Dendrobium crumenatum (Tropical pigeon orchid).

Q84LA2
ID Q84LA2 PRELIMINARY; PRT; 370 AA.
AC Q84LA2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S-adenosylmethionine decarboxylase.
GN Name=Samdc;
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=4-day old flower tepals;
RA Gookin T.E., Cabauatan E.V., Hunter D.A., Reid M.S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232672; AAC043186.1; -.
DR HBL; P17707; IJEN.
DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spERMINE biosynthesis; IEA.
DR GO; GO:0006597; P:spERMINE biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 370 AA; 40680 MW; 36F619BA4806F70F CRC64;

Query Match 60.8%; Score 1187.5; DB 2; Length 370;
Best Local Similarity 58.7%; Pred. No. 1.3e-88;
Matches 224; Conservative 58; Mismatches 50; Indels 48; Gaps 4;

Qy 13 SAIGFEGYKRLTTFSEAPVFDVPHGSGRLALRSQIDSVLDLAR----- 58
Db 4 SPIGFEGYKRLTTFSEAPVFDVPHGSGRLALRSQIDSVLDLARCTIVSLSNKHFD 63
Qy 59 -----KIVIKTCGTTKLLTIPRILELAELSMPLAAYKYSRGTFIPGAQP 105
Db 64 YVLSSESLFYPCMKILKTCGTTLLLSIPVILDLAELSLSVTAVKYSRGTFIPGAQP 123
Qy 106 AHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPGQKHYYATYEPPEPMVNLKMT 165
Db 124 AHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPGQKHYYATYEPPEPMVNLKMT 183
Qy 166 GLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDFPCGYSMNAIHGSF 225
Db 184 GLNTEKASIFKNSVPRHSSAKEMTKRSGICDIIPEMKICDFDFPCGYSMNGINKAL 243
Qy 226 STIHVTPEDGFSYASVEVWGLDATALSYGLVKRVLCGFPSPFSVAVTIFGGRGQAGTW 285
Db 244 STIHVTPEDGFSYASVEAMGNFAELDFGGLVERVLECFGPAFDSVAVTIFGGRGQAGSW 303
Qy 286 GKELGAEAYDCNNMVDELPGGGLIYQSCAAEDAVASSPKSVLRFCFDGENAAPPKDC 345
Db 304 GKQVSVNGYCNKLVQDLGGGLIYQSFKASDGG-SASPRSLYCWAE-----AED- 356
Qy 346 KLANVLCLEEXDAIEEK 365
Db 357 -----EEENG 362

RESULT 11
Q9FSM2
ID Q9FSM2 PRELIMINARY; PRT; 319 AA.
AC Q9FSM2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE S-adenosylmethionine decarboxylase.
GN Name=H0711G06.28;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Peng Q., Mu J., Zhou B., Chen Z.H., Li Y., Zhu J.J.,
RA Tang Y.S., Zhao Q., Liu Y.L., Huang Y.C., Yu Z., Fan D.L., Chen L.,
RA Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X.,
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RA Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
 RA Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.,
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL442115; CAC09522.1; --
 DR HSP; P17707; I17B.
 DR Gramene; Q9F8M2; --
 DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spermine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_Dcase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 SQ SEQUENCE 319 AA; 34854 MW; B0648B852F7A4A61 CRC64;
 Query Match 59.38; Score 1134.5; DB 2; Length 319;
 Best Local Similarity 80.28; Pred. No. 1.5e-86;
 Matches 223; Conservative 10; Mismatches 18; Indels 27; Gaps 1;
 QY 1 MAVLSAAGAPPASAIPEGYEKRLIITFSEAPVFDVPHGSLRALRSQIDSVLDLAR-- 58
 DB 37 MGVLAAADPPVPSAIPEGYEKRLIITFSEAPVFDVPHGSLRALRSQIDSVLDLARCT 96
 QY 59 -----KIVIKTGGTKLLLTIPRILELAELSMPLAAYKY 93
 DB 97 IVSELSNKDPSVYLSSESLFIYSKIVIKTGGTKLLLTIPRILELAELSMPLAAYKY 156
 QY 94 SRGTFFPGQAPAPHRFSFSEAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYATEYP 153
 DB 157 SRGMFIFFSQAAPHRFSFSEAVLNRYFGHLKSGGNAYVIGDPAKPGQKWHIYYATQHP 216
 QY 154 EQPMVNLKMTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDPEPC 213
 DB 217 EQPMVNLKMTGLDTRKASVFFKTSADGHTSCAKEMTKLSGISIIPEMEICDFDPEPC 276
 QY 214 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVVGLDATAL 251
 DB 277 GYSNNAIHGLAFSTIHTVPEDGFSYASYEVVGLDALL 314
 RESULT 12
 QYXZQ9 PRELIMINARY; PRT; 358 AA.
 AC QYXZQ9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50).
 GN Name=samdc;
 OS Vitis vinifera (Grape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Vitaceae; Vitis.
 OX NCBI_TaxID=29760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Tassoni A., Accetulli P., Bagni N.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ567368; CAB98785.1; --
 DR HSP; P17707; IJEN.
 DR GO; GO:0004014; P:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spermine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_Dcase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 KW Lyase.
 FT CHAIN 2 358 S-adenosylmethionine decarboxylase.

SQ SEQUENCE 358 AA; 39783 MW; B6037EDA79132AE3 CRC64;
 Query Match 44.8%; Score 858; DB 2; Length 358;
 Best Local Similarity 50.6%; Pred. No. 2.4e-63;
 Matches 182; Conservative 50; Mismatches 78; Indels 50; Gaps 8;
 QY 9 APPASAIPEGYEKRLIITFSEAPVFDVPHGSLRALRSQIDSVLDLAR----- 58
 DB 2 ALPVSAIPEGYEKRLIITFSEAPVFDVPHGSLRALRSQIDSVLDLAR----- 61
 QY 59 -----KIVIKTGGTKLLLTIPRILELAELSMPLAAYKYSGRTFFP 101
 DB 62 IVDSYVLSSESLFVYPYKIIITCGTTKLLLTIPRILELAELSMPLAAYKYSGRTFFP 121
 QY 102 GAQAPHRFSFSEAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIY-YATEYP--EQPMV 158
 DB 122 GAQYPRHFSFSEAVLDGHGELGAGSKAYMWSHDKP-QKWHVYTAATAAFTGRSDPY 180
 QY 159 NLEMCWTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDPEPCGYSMN 218
 DB 181 TLEMCWTGLDTRKASVFFKTT-----DTSSAAVMTENGIRKILPNSICDFEPCGYSMN 236
 QY 219 AIHGSASFSTIHTVPEDGFSYASYEVVGLDATALSYGDLVKRVLGCGSPFSFSAVTIFGG 278
 DB 237 AIEGAISTIHTVPEDGFSYASFTVGNPKVNLHSLIERVLSFCQPNFESVAV----- 291
 QY 279 RGQAGTWGK-----ELGAEAYDCNNNVEOELPGGTLIIYQSCFAEDAVASPSKVLRC 332
 DB 292 --HADISGKLLERCLLDVKGCCERSNEELGMCSSMYHREMKTEGLV--SPRSILKC 347
 RESULT 13
 DCAM CATRO
 ID DCAM CATRO STANDARD; PRT; 357 AA.
 AC Q42679;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
 DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
 GN Name=SAMDC;
 OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae;
 OC Catharanthus.
 OX NCBI_TaxID=4058;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-71.
 RX MEDLINE=95188916; PubMed=7883014;
 RA Schroeder G., Schroeder J.;
 RT "cDNAs for S-adenosyl-L-methionine decarboxylase from Catharanthus roseus, heterologous expression, identification of the proenzyme-processing site, evidence for the presence of both subunits in the active enzyme, and a conserved region in the 5' mRNA leader.";
 RL Eur. J. Biochem. 228:74-78(1995).
 CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -|- COFACTOR: Pyruvoyl group.
 CC -|- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
 CC -|- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
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 CC -----


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DR EMBL; U12573; AAC48989.1; -.
DR PIR; S68990; S68990.
DR HSP; P17707; IJEN.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 70
FT S-adenosylmethionine decarboxylase beta
FT chain.
FT CHAIN 71 357
FT S-adenosylmethionine decarboxylase alpha
FT chain.
FT SITE 70 71
FT Cleavage (nonhydrolytic).
FT MOD_RES 71 71
FT Pyruvic acid (Ser).
FT ACT_SITE 11 11
FT By similarity.
FT ACT_SITE 14 14
FT By similarity.
FT ACT_SITE 85 85
FT By similarity.
FT MUTAGEN 71 71
FT S->A: Loss of activity.
SQ SEQUENCE 357 AA; 39714 MW; 364918E116388301 CRC64;

Query Match 44.6%; Score 854.5; DB 1; Length 357;
Best Local Similarity 47.6%; Pred. No. 4.8e-63;
Matches 185; Conservative 52; Mismatches 83; Indels 69; Gaps 8;

QY 9 APPASAIIGPGYKRLIETSEAPVFDVPHGSGLRALSRQIDSVLRLAR----- 58
DB 2 ALPASAIGFGYKRLIETSEAPVFDVPHGSGLRALSRQIDSVLRLAR----- 61
QY 59 -----KIVIKTCGTTKLLTTPRILELAELSMPAAVKYSGRTFIFP 101
DB 62 YLDSYVLSSESLFVYKIIKTCGTTKLLTTPRILELAELSMPAAVKYSGRTFIFP 121
QY 102 GAGAPHRSESEVAVLNRYFGGLKSGGNAYVIGDAARPCQKHYYATYPRQ----PMV 158
DB 122 GAQSFPHRSSESEVELLDNDFGKLGSNAFINGNDPQP-QKWHVXSASVGSQSDPTY 180
QY 159 NLEMCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPEMETICDFPFCGYSMN 218
DB 181 TLEMCMTGLDREKASVFFK-----ESSAALMTSRGIRKILPDSEICDFPFCGYSMN 236
QY 219 AIHGSFSTHVTPEGFSYASVEVMGLDATALSYGLVKRVLCGFGSPFSFVAVTIFGG 278
DB 237 SIEEAISTHVTPEGFSYASFEAGYDLKAQNLGMIERVLACFPSEFSVAV----- 291
QY 279 RGOAGTWK-----ELGABAYDCNNVVEQLPGGILLIYQSCAAEDAVASSPKSVLRC 332
DB 292 --HCDVTCKSLQICSLKEYSLDEKINEELGLGSIYKFKLRID--ACGSPRSILKC 347
QY 333 FDGENAAPFAKCKLANLVGLEEXDALEE 361
DB 348 -----CWKEDESEEE 357

RESULT 14
DCAM_VICFA STANDARD; PRT; 353 AA.
AC Q9M4DB;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdometDC)
DE (samDC) [contains: S-adenosylmethionine decarboxylase alpha chain; S-
DE adenosylmethionine decarboxylase beta chain].
GN Name=sAMDC;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Kleine Thueringer; TISSUE=Root nodules;
```

```
RA Fruehling M., Puehler A., Perlick A.M.;
RT "Isolation and characterization of a full-length cDNA encoding S-
RT adenosylmethionine decarboxylase from broad bean (Vicia faba L.).";
RL (er) Plant Gene Register PGR00-029.
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-
CC adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -|- COFACTOR: Pyruvoyl group (By similarity).
CC -|- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -|- SIMILARITY: Belongs to the eukaryotic AdometDC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ250026; CAB76966.1; -.
DR HSP; P17707; IJEN.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 68
FT S-adenosylmethionine decarboxylase beta
FT chain (By similarity).
FT CHAIN 69 353
FT S-adenosylmethionine decarboxylase alpha
FT chain (By similarity).
FT SITE 68 69
FT Cleavage (nonhydrolytic) (By similarity).
FT MOD_RES 69 69
FT Pyruvic acid (Ser) (By similarity).
FT ACT_SITE 9 9
FT By similarity.
FT ACT_SITE 12 12
FT By similarity.
FT ACT_SITE 83 83
FT By similarity.
SQ SEQUENCE 353 AA; 38512 MW; 90AB36A7FE0F0454 CRC64;

Query Match 44.5%; Score 851; DB 1; Length 353;
Best Local Similarity 50.1%; Pred. No. 9.3e-63;
Matches 178; Conservative 48; Mismatches 91; Indels 38; Gaps 6;

QY 13 SAIGFPGYKRLIETSEAPVFDVPHGSGLRALSRQIDSVLRLAR----- 55
DB 4 SAIGFPGYKRLIETSEAPVFDVPHGSGLRALSRQIDSVLRLAR----- 63
QY 56 -----LARKIVIKTCGTTKLLTTPRILELAELSMPAAVKYSGRTFIFGQAP 105
DB 64 YVLSSESLFVYKIIKTCGTTKLLTTPRILELAELSMPAAVKYSGRTFIFGQAP 123
QY 106 APHRSSESEVAVLNRYFGGLKSGGNAYVIGDAARPCQKHYYATY-----YPEQPMVNL 162
DB 124 FPHRFSESEVAVLDGFGKLGSGKAYIMG-GSDEAQNHVYCASADSVPADSVYTLEM 182
QY 163 CMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISIIPEMETICDFPFCGYSMAIHG 222
DB 183 CMTGLDREKASVFFK-----QTGSAABMTVNSGIRKILPNSIICDFPFCGYSMSVEG 238
QY 223 SAFSTHVTPEGFSYASVEVMGLDATALSYGLVKRVLCGFGSPFSFVAVTIFGGRQA 282
DB 239 PAVSTHVTPEGFSYASVETAGYDLKAMNLNEMVMRLACFPQTFEFSVAVH-DNASKS 297
QY 283 GTWKGELGABAYDCNNVVEQLPGGILLIYQSCAAEDAVASSPKSVLRCFDGEN 337
DB 298 FEQGCILLDVKGCCDEKSHQGLGMSGVVYKQFVKASD--CGSPRSTLCKWKDED 350

RESULT 15
DCAM_SPIOL STANDARD; PRT; 363 AA.
AC P46255;
DT 01-NOV-1995 (Rel. 32, Created)
```

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
DE adenosylmethionine decarboxylase beta chain].
GN Name=SAMDC;
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Monatol;
RC MDLINE=95288374; PubMed=7770535; DOI=10.1104/pp.107.4.1461;
RA Bolle C., Hermann R.G., Oelmüller R.;
RT "A spinach cDNA with homology to S-Adenosylmethionine decarboxylase";
RL Plant Physiol. 107:1461-1462(1995).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S)-deoxy-5-
CC adenosyl(3-aminopropyl)-methylsulfonium salt + CO(2).
CC -1- COFACTOR: Pyruvoyl group (By similarity).
CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X81414; CA57170.1; -;
DR PIR; S49222; S49222.
DR HSP; P17707; IJEN.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 68 S-adenosylmethionine decarboxylase beta
FT chain (By similarity).
FT CHAIN 69 363 S-adenosylmethionine decarboxylase alpha
FT chain (By similarity).
FT SITE 68 69 Cleavage (nonhydrolytic) (By similarity).
FT MOD_RES 69 69 Pyruvic acid (Ser) (By similarity).
FT ACT_SITE 9 9 By similarity.
FT ACT_SITE 12 12 By similarity.
FT ACT_SITE 83 83 By similarity.
SQ SEQUENCE 363 AA; 39959 MW; CE4D6DDE4E8A3220 CRC64;
Query Match 43.9%; Score 841; DB 1; Length 363;
Best Local Similarity 46.6%; Pred. No. 6.6e-62;
Matches 184; Conservative 45; Mismatches 86; Indels 80; Gaps 9;
QY 13 SAIGFEGYKRLRITTFSEAPVFVDPHGSLRALSRQIDSVDL----- 55
DB 4 SAIGFEGYKRLRITTFSEAPVFVDPHGSLRALSRQIDSVDL----- 55
QY 56 -----LARKIVIKTGTGTTKLLTIPRIELAEELSMPLAAVKYSGTTFPCAOP 105
DB 64 YVLSSESLFYAYKIIKTCGTTKLLRAIPPLRLAGKSLDVKSRYTRGSFIFPGAQS 123
QY 106 APRHSFSEEVAVLNRYFGGLKSGGNVYVIGDAPRGOKWHIYATEYP---EOPMVNLEM 162
DB 124 YAHRSFSEEVAVLDGYFGKLAAGSKAFVWGDPKAP-QXNVHVSASAEITISFEFVYILEM 182
QY 163 CMTGLDTKASVFVKTNADGNNTTCAKEMTKLSGISEIIPEMEICDPDFPCGYSMNAIHG 222
DB 183 CMTGLKKEKASVFFKSPN-----AAVMTESSGIRKILPDKICDPDFPCGYSMNAIEG 238

QY 223 SAFSTIHTVPEDGFSYASVEVMGLDATALSYGDLVRRVLGCGFPGSEFSVAVTIFGGRGQA 282
DB 239 PAISTTIHTPEDGFSYASFEAVGYDLKTKDNLQNLVERVLACFPSPSEFSIAI----- 289
QY 283 GTWKGELGAPAYDCNNWVE-----QELP-GGGIILYQSFCAAED--AVASSPKS 328
DB 290 ---HAEIAANSMEHNCYVNVNGYSRBEGGIEELGFGAASVYQKFKCASTGFGATNPKP 346
QY 329 VLRCFDGENAAPFAKDKCLANLYCLEEXDAIEBKD.363
DB 347 ALKC-----CWKEDKFEFEKD 362

Search completed: May 11, 2005, 22:52:29
Job time : 87.9416 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:42:53 ; Search time 19.6014 Seconds
(without alignments)
1806.392 Million cell updates/sec

Title: US-10-732-923-407

Perfect score: 1914

Sequence: 1 MAVLSAAGAPPASAIQFEGY.....NLVCLREXDAIEKQGVLD 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1726	90.2	400	2 T03947	adenosylmethionine
2	1520	79.4	398	2 T04099	adenosylmethionine
3	1472.5	76.9	393	2 S69191	adenosylmethionine
4	854.5	44.6	357	2 S68990	adenosylmethionine
5	841	43.9	363	2 S49222	adenosylmethionine
6	837.5	43.8	361	2 T01934	adenosylmethionine
7	834	43.6	353	2 T06515	probable adenosylm
8	825.5	43.1	381	2 T10707	adenosylmethionine
9	824.5	43.1	377	2 T10708	adenosylmethionine
10	822.5	43.0	360	2 S52662	adenosylmethionine
11	763.5	39.9	361	2 T12613	adenosylmethionine
12	757	39.6	362	2 T51378	adenosylmethionine
13	751	39.2	369	2 T10750	probable adenosylm
14	377.5	19.7	368	2 T22361	adenosylmethionine
15	359.5	18.8	334	1 DCHYDM	adenosylmethionine
16	357.5	18.7	334	2 A55948	adenosylmethionine
17	356.5	18.6	334	1 DCHUDM	adenosylmethionine
18	351.5	18.4	333	1 DCRITM	adenosylmethionine
19	337.5	17.6	335	2 S72197	adenosylmethionine
20	294	15.4	396	1 DCBYDM	adenosylmethionine
21	99.5	5.2	2297	2 T34918	polyketide synthas
22	96.5	5.0	410	2 AH3376	glycosyltransferas
23	95.5	5.0	357	2 JQ0118	acyl-CoA-6-aminope
24	94.5	4.9	1307	2 T35944	probable beta-gala
25	90.5	4.7	689	2 F81286	probable polysacch
26	90.5	4.7	3972	2 S75251	hypothetical prote
27	90	4.7	288	2 H95274	probable ABC trans
28	90	4.7	1354	2 T13363	phosphoribosylform
29	89.5	4.7	656	2 A33483	dnaK-type molecula

30 89 4.6 255 2 H75074 lactam utilization
31 89 4.6 774 2 B84031 ATP-dependent prot
32 88.5 4.6 719 2 A42808 Ig light chain-bin
33 88 4.6 352 2 C90547 oligopeptide ABC t
34 88 4.6 355 2 T50566 probable ABC-type
35 88 4.6 433 2 T36609 probable secreted
36 88 4.6 983 2 AG2381 glycine cleavage s
37 87.5 4.6 255 1 E71090 probable lactam ut
38 87.5 4.6 759 2 T37499 probable formate d
39 87 4.5 534 2 B97352 polygalacturonase
40 86.5 4.5 739 2 H72364 aspartokinase II -
41 86.5 4.5 1397 2 A85570 rhaC protein in rh
42 86.5 4.5 1397 2 C64805 rhaC protein precu
43 86.5 4.5 1431 2 A45866 dextranucrase (EC
44 86 4.5 355 2 F69298 conserved hypotet
45 86 4.5 374 2 C91198 BspD protein limpo

ALIGNMENTS

RESULT 1

T03947

adenosylmethionine decarboxylase (EC 4.1.1.50) - maize

N;Alternate names: S-adenosylmethionine decarboxylase

C;Species: Zea mays (maize)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T03947

R;Michael, A.J.

submitted to the EMBL Data Library, September 1996

A;Reference number: Z15155

A;Accession: T03947

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-400 <MIC>

A;Cross-references: UNIPROT:O24575; EMBL:Y07767; PIDN:CAA69075.1

C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase

F;78/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 90.2%; Score 1726; DB 2; Length 400;
Best Local Similarity 84.5%; Pred. No. 2.5e-135;
Matches 338; Conservative 8; Mismatches 22; Indels 32; Gaps 3;

Qy	1	MAVLSAAGAPPASAIQFEGYEKLEITFSEAPVFPVPHGSLRALSRQSDSVLDLAR--	58
Db	1	MAVLSAADASPVSAIQFEGYEKLEITFSEAPVFPVPHGSLRALSRQSDSVLDLARCT	60
Qy	59	-----XIVIKTCGTTKLLLTIPRILELAELSMPAAVKY	93
Db	61	IVSELNKKDFSVYLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKY	120
Qy	94	SRGTFTFPQAQPHRSPSEVAVLNRYFGCLSGGNAYVIGDAARQKWHIYATEYP	153
Db	121	SRGTFTFPQAQPHRSPSEVAVLNRYFGCLSGGNAYVIGDPAREGQKWHVYATEYP	180
Qy	154	EQPMVNLNEMCMTGLDTKKASVFEKTNADGNNTTCAKEMTKLSGISEIIPENIEICDPDEPC	213
Db	181	EQPMVNLNEMCMTGLDKKKACVFFKTNADGNNTTCAKEMTKLSGISEIIPENIEICDPDEPC	240
Qy	214	GYSMNAIHGSAFTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGFSEFSVAV	273
Db	241	GYSMNAIHGSAFTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGFSEFSVAV	300
Qy	274	TIFGGRGAGTGWKELGAEAYDCNNMVVEQLPGGGLIYOSFCAEDAVASSPKSVURCF	333
Db	301	TIFGGRGAGTGWKELGAEAYDCNNMVVEQLPGGGLIYOSFCAEDAVASSPKSVURCF	360
Qy	334	DGENA----APPADCKLANLVCL-REXDAIEEKQGVLD 368	
Db	361	DGENVSAPPMMKKDYKLANLLCWEEADANEKAGVLDE 400	

```
RESULT 2
T04099
adenosylmethionine decarboxylase homolog [similarity] - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Mar-2004
C;Accession: T04099
R;Michael, A.J.
submitted to the EMBL Data Library, September 1996
A;Description: Spermidine biosynthesis in rice.
A;Reference number: Z15210
A;Accession: T04099
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-398 <MC>
A;Cross-references: EMBL:Y07766; PIDN:CAA69074.1
A;Experimental source: cv. Nipponbare
A;Note: this sequence appears to lack the residues necessary to form an active site
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type

Query Match      79.4%; Score 1520; DB 2; Length 398;
Best Local Similarity 76.5%; Pred. No. 3e-118;
Matches 306; Conservative 18; Mismatches 42; Indels 34; Gaps 5;

Qy 1 MAVLSAAGAPPASAIPEGYKRLIITFSEAPVFDVPHGSGRLALSRQIDSVLDLAR-- 58
Db 1 MGDLSAADPPVSAIPEGYKRLIITFSEAPVFDVPHGSGRLALSRQIDSVLDLARCT 60
Qy 59 -----KIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKY 93
Db 61 IVSELSNKDFSVLLSPACLSILIKIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKY 120
Qy 94 SRGTIFPGQAPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEYP 153
Db 121 SRGMFIFFSAQAPLRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATQHP 180
Qy 154 EQPMVNLMECMTGLDITKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDPEPC 213
Db 181 EQPMVNLMECMTGLDITKASVFFKTSADGHTSCAKEMTKLSGISIIPMEICDFDPEPC 240
Qy 214 GYSNNAIHGSAFSTIHTVPDGFSGYASYEVNGLDATALSVDLVKRVLCGFGSPSEFSVAV 273
Db 241 GYSNNAIHGSAFSTIHTVPDGFSGYASYEVNGLDATALSVDLVKRVLCGFGSPSEFSVAV 300
Qy 274 TIFGGRQAGTWKELCAEAYDCNNMVEQELPGGILLIYQSFCAED--AVASPKSVLR 331
Db 301 TIFGGHGHAGTWKELNADAYKCNMVEQELPGGILLIYQSFCAEDVDPVAVGSPKSVLH 360
Qy 332 CFDGE---NAAPFAKCKLANLVCLLEKDAIEEKDGVLD 368
Db 361 CFEAENMNPAP-VKEGKLGNNLPWGE-DALENDGVFDE 398

RESULT 3
S69191
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - wild barley
C;Species: Hordeum chilense (wild barley)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69191
R;Dresselhaus, T.; Barcelo, P.; Hagel, C.; Loerz, H.; Humbeck, K.
Plant Mol. Biol. 30, 1021-1033, 1996
A;Title: Isolation and characterization of a Tritordeum cDNA encoding S-adenosylmethionine
A;Reference number: S69191; MUID:96270379; PMID:8639739
A;Accession: S69191
A;Molecule type: mRNA
A;Residues: 1-393 <DRE>
A;Cross-references: UNIPROT:Q42829; EMBL:X83881; NID:g1403043; PIDN:CAA58762.1; PID:g140
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;1-71/Product: adenosylmethionine decarboxylase beta chain #status predicted <Mat1>
F;72-393/Product: adenosylmethionine decarboxylase alpha chain #status predicted <Mat2>
F;247-262/Region: PEST sequence
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted
```

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Query Match      76.9%; Score 1472.5; DB 2; Length 393;
Best Local Similarity 74.6%; Pred. No. 2.6e-114;
Matches 290; Conservative 25; Mismatches 43; Indels 31; Gaps 4;

Qy 9 APPASAIPEGYKRLIITFSEAPVFDVPHGSGRLALSRQIDSVLDLAR----- 58
Db 2 AAPVASIPEGYKRLIITFSEASIFADPHGRGLRALSRQIDSVLDLARCTIVSELSNK 61
Qy 59 -----KIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKYRGRTIFFP 101
Db 62 DFDSYVLSSESLFIYQKIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKYRGRTIFFP 121
Qy 102 GAOPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEVPQPMVNL 161
Db 122 GAOPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEVPQPMVNL 181
Qy 162 MCMTGTDITKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDPEFCGYSMNAIH 221
Db 182 MCMTGTDITKASVFFKTHADGHVCAKEMTKLSGISIIPMEICDFDPEFCGYSMNAIN 241
Qy 222 GSASFSTIHTVPDGFSGYASYEVNGLDATALSVDLVKRVLCGFGSPSEFSVAVIFGGRQ 281
Db 242 GSASFSTIHTVPDGFSGYASYEVNGLDATALSVDLVKRVLCGFGSPSEFSVAVIFGGRGH 301
Qy 282 AGTWKELGAEAYDCNNMVEQELPGGILLIYQSFCAEDAV--ASSPKSVLRCFDG-ENA 338
Db 302 AATWKGKLDAAEDCNMVEQELPGGILLIYQSFCAEDAV--ASSPKSVLRCFDG-ENA 361
Qy 339 APPAKCKLANLVCLLEKDAIEEKDGVLD 366
Db 362 HPLVKEGKLANLLAWRAEESLEEGTGAL 390

RESULT 4
S68990
adenosylmethionine decarboxylase (EC 4.1.1.50) - Madagascar periwinkle
N;Alternate names: S-adenosyl-L-methionine decarboxylase proenzyme
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S68990
R;Schroeder, G.; Schroeder, J.
Eur. J. Biochem. 228, 74-78, 1995
A;Title: cDNAs for S-adenosyl-L-methionine decarboxylase from Catharanthus roseus, hetero-
in the active enzyme, and a conserved region in the 5' mRNA leader.
A;Reference number: S68989; MUID:95188916; PMID:7883014
A;Accession: S68990
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-357 <SCH>
A;Cross-references: UNIPROT:Q42679; EMBL:U12573; NID:g758693; PID:g758695
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;71/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match      44.6%; Score 854.5; DB 2; Length 357;
Best Local Similarity 47.6%; Pred. No. 4e-63;
Matches 185; Conservative 52; Mismatches 83; Indels 69; Gaps 8;

Qy 9 APPASAIPEGYKRLIITFSEAPVFDVPHGSGRLALSRQIDSVLDLAR----- 58
Db 2 ALPASAIPEGYKRLIITFSEAFADPDGKGLRALNKQIDLEILPAEACTIVDSLSNQ 61
Qy 59 -----KIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKYRGRTIFFP 101
Db 62 YLDSYVLSSESLFIYQKIVIKTCGTTKLLLTIPRILELAELSMPPLAAVKYRGRTIFFP 121
Qy 102 GAOPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEVPEO---PMV 158
Db 122 GAOPAPHRFSSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHIYYATEVPEO---PMV 180
Qy 159 NLEMCMTGTDITKASVFFKTNADGNTTCAKEMTKLSGISIIPMEICDFDPEFCGYSMN 218
Db 181 TLEMCMTGTDITKASVFFKTSADGHTSCAKEMTKLSGISIIPMEICDFDPEFCGYSMN 236
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Db 64 YVLSSESLFVYAYKLIITCGTCTKLLSIPPTLKADISILNVRSVRYTRGSFIFFPGAQS 123
 QY 106 APHRSFSEEVAVLNRYFGLKSGGNVAYIGDAARPGQKWHIYYATE--YPEQPMVNLEM 162
 Db 124 FPHRFSEEVAVLGGFFKLGSGSNWAYILG-GSDAQNWHIYCASDSVSPGSGVTLEM 182
 QY 163 CMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISIIPMEMEICDFDFEPCGYSMNAIHG 222
 Db 183 CMTGLDREKASVFKE-----QTGSAAEVTNSGIRKILRNSEICDFDFEPCGYSMNSVVG 238
 QY 223 SAFSTIHVTPDGRFSYASYEVWGLDATLSYGDVLKRVLGCGRPSSEFSVAVTIFGGRGQA 282
 Db 239 SAVSTIHVTPDGRFSYASFETAGYDLKAINLNMVNRVLACFPQTEFSVAVHV-DNASKS 297
 QY 283 GTWCKELGAEAYDCNNMVEQLPGCGILLYQSCFAEADAVASSPSKSLVRCFPGEN 337
 Db 298 FEQGLLDVKGCCBEKSHOGLMGSGVVYQKF--LKTSYCGSPRSTLKCKWDED 350

RESULT 8
 T10707
 adenosylmethionine decarboxylase (EC 4.1.1.50) 1 - clove pink
 N:Alternate names: S-adenosylmethionine decarboxylase 1
 C:Species: Dianthus caryophyllus (clove pink)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T10707; T10787
 R:Lee, M.M.; Lee, S.H.; Park, K.Y.
 submitted to the EMBL Data Library, October 1995
 A:Description: Nucleotide sequence of cDNAs encoding S-adenosylmethionine decarboxylase from *Dianthus caryophyllus* (clove pink).
 A:Reference number: Z17089
 A:Accession: T10707
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-381 <LEE>
 A:Cross-references: UNIPROT:Q39676; EMBL:U38526; NID:G1155239; PID:g1155240
 A:Experimental source: cv. White Sim; carnation petal
 R:Kim, Y.J.; Lee, M.M.; Chang, K.S.; Lee, S.H.; Park, K.Y.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: Z17144
 A:Accession: T10787
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-381 <KIM>
 A:Cross-references: EMBL:U94786; NID:G2406584; PID:g2406585
 A:Experimental source: strain White sim
 C:Genetics:
 A:Gene: gcsadc9
 C:Function:
 A:Description: catalyzes the decarboxylation of S-adenosyl-L-methionine to (S)-adenosyl-L-homocysteine
 A:Pathway: polyamine biosynthesis
 C:Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
 C:Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
 F:93/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 43.1%; Score 825.5; DB 2; Length 381;
 Best Local Similarity 48.3%; Pred. No. 1.1e-60;
 Matches 180; Conservative 46; Mismatches 86; Indels 59; Gaps 8

QY 13 SAIGFEGYKRLKLEITFSEAPVFDVPHGSLGRALSQDLSVLDLAR----- 58
 Db 28 SAIGFEGFEKRLKLEISFPEGIFVDPEGGLRALSQAQLDEILGPAECTIVDSLANSVDS 87
 QY 59 -----KIVIKTCGTTKLLLTIPRILEAEBSLWPLAAVKYRGTFIFPGAQP 105
 Db 88 YVLSSESLFVYSYKIIITCGTCTKLLHSILPILTLADGLCLDVKSVRYTRGSFIFFPGAQS 147
 QY 106 APHRSFSEEVAVLNRYFGLKSGGNVAYIGDAARPGQKWHIYYATEYP--EOPMVNLEM 163
 Db 148 YPHRSFSEEVAVLDKYFNLGTGSKAFVWNGSPAKP-QKWHVYSATAEFSYDDPVVLEMC 206
 QY 164 MTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISIIPMEMEICDFDFEPCGYSMNAIHGS 223

S52662
adenosylmethionine decarboxylase (EC 4.1.1.50) TUB13 [similarity] - potato
C;Species: Solanum tuberosum (potato)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52662; S28047
R;Arif, S.A.M.; Taylor, M.A.; George, L.A.; Butler, A.R.; Burch, L.R.; Davies, H.V.; Sta
Plant Mol. Biol. 26, 327-338, 1994
A;Title: Characterisation of the S-adenosylmethionine decarboxylase (SAMDC) gene of pota
A;Reference number: S52662; MUID:95036004; PMID:7948879
A;Accession: S52662
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <ARI>
A;Cross-references: UNIPROT:Q04694; GB:S74514; NID:G807093; PIDN:AA32507.1; PID:G807094
R;Taylor, M.A.; Arif, S.A.M.; Kumar, A.; Davies, H.V.; Scobie, L.A.; Pearce, S.R.; Flav
Plant Mol. Biol. 20, 641-651, 1992
A;Title: Expression and sequence analysis of cDNAs induced during the early stages of tu
A;Reference number: S28046; MUID:93081725; PMID:1450379
A;Accession: S28047
A;Molecule type: mRNA
A;Residues: 1-173, 'S', '175-256, 'T', '258-290, 'V', '292-304, 'I', '306-360 <TAY>
A;Cross-references: EMBL:Z11680; GB:S51455; NID:G21484; PIDN:CAA7742.1; PID:G21485
C;Genetics:
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;73/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 43.0%; Score 822.5; DB 2; Length 360;
Best Local Similarity 48.5%; Pred. No. 1.8e-60;
Matches 176; Conservative 48; Mismatches 88; Indels 51; Gaps 8;
QY 11 PASAIGFEGEYKRLITFSEAPVFDVPHGSGRLRALSQIDSVLDLAR----- 58
DB 6 PVAIGFEGEYKRLITFSEAPVFDVPHGSGRLRALSQIDSVLDLAR----- 58
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTTFIPPGA 103
DB 66 DSVLSESSLFVYVYKIIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTTFIPPGA 125
QY 104 QPAPHRSPSEVAVLNRYFGLKSGGNAYVIGDAARPGQKHYYATEYPEQ----PMVNL 160
DB 126 QSPFHRHSEVAVLDYFGKLAAGSAVIMGSPDKT-QKHVYASAGVQSNDFPYTL 184
QY 161 EMCWTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSNNAI 220
DB 185 EMCWTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSNNAI 240
QY 221 HGSAFSTIHTVPEDGFSYASVYMGDLATALSVDLVRKVLGCGFSPSEFSAVTFIFGGR 280
DB 241 EGAAVSTIHTVPEDGFSYASVYMGDLATALSVDLVRKVLGCGFSPSEFSAVTFIFGGR 293
QY 281 QAGTWGK-----ELGAEAYDCNNVWEQELPGGGLIYQSFCAEDAVASPKSVLR-QF 333
DB 294 HADVATKLLERTCSVDVKYSLAWESEPEFEGGSIYVQKFP--TRTPCYSPKSVLKGCV 351
QY 334 DGE 336
DB 352 KEE 354

RESULT 11
T12613
adenosylmethionine decarboxylase (EC 4.1.1.50) - common sunflower
N;Alternate names: S-adenosylmethionine decarboxylase
C;Species: Helianthus annuus (common sunflower)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12613
R;Eliasson, A.; Hamman, P.; Steinmetz, A.
Submitted to the EMBL Data Library, May 1998
A;Description: Coding sequence for an S-adenosylmethionine decarboxylase from sunflower
A;Reference number: Z17552
A;Accession: T12613

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-361 <BLI>
A;Cross-references: UNIPROT:O65354; EMBL:AF066078; NID:G3153905; PID:G3153906
A;Experimental source: cultivar HA300; mature pollen
C;Genetics:
A;Gene: SAD
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 39.9%; Score 763.5; DB 2; Length 361;
Best Local Similarity 48.1%; Pred. No. 1.4e-55;
Matches 177; Conservative 49; Mismatches 87; Indels 55; Gaps 12;
QY 13 SAIGFEGEYKRLITFSEAPVFDVPHGSGRLRALSQIDSVLDLAR----- 58
DB 3 SAIGFEGEYKRLITFSEAPVFDVPHGSGRLRALSQIDSVLDLAR----- 58
QY 59 -----KIVIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTTFIPGAQP 105
DB 63 YVLSSESLFVYVYKIIKTCGTTKLLTIPRILELAELSMPAAVKYSGRTTFIPGAQP 122
QY 106 AHRSPSEVAVLNRYFGLKSGGNAYVIGDAARPGQKHYYATEYPEQ-----PMVN 159
DB 123 FPHRSFTEEVMLDSHFGLKSGGNAYVIGDAARPGQKHYYATEYPEQ-----PMVN 181
QY 160 LEMCMTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSNNA 219
DB 182 LEMCMTGLDTRKASVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSNNA 237
QY 220 IHGSAFSTIHTVPEDGFSYASVYMGDLATALSVDLVRKVLGCGFSPSEFSAVTFIFGGR 279
DB 238 IEGDAISTIHTVPEDGFSYASVYMGDLATALSVDLVRKVLGCGFSPSEFSAVTFIFGGR 295
QY 280 QAGTWGKELGABAYDCN-----NMVE---QELPG-GLIYQSFCAEDAVASPKSVL- 330
DB 296 NVV-----KOLNLENNVNVKGVNVEETKEVLEGGGSMVYVGF-ARGGSCGSPRSTLH 350
QY 331 RCF-DGEN 337
DB 351 RCF-DGEN 358

RESULT 12
T51378
adenosylmethionine decarboxylase (EC 4.1.1.50) [similarity] - Arabidopsis thaliana
N;Alternate names: protein FIN13_90
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51378
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Ban
Submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-362 <SAT>
A;Cross-references: UNIPROT:Q9S779; EMBL:AL391145
A;Experimental source: cultivar Columbia; BAC clone FIN13
C;Genetics:
A;Map position: 5
A;Note: FIN13_90
C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
F;69/Cleavage site: Glu-Ser (autolytic) #status predicted
F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 39.6%; Score 757; DB 2; Length 362;
Best Local Similarity 45.6%; Pred. No. 4.9e-55;
Matches 170; Conservative 52; Mismatches 97; Indels 54; Gaps 9;
QY 13 SAIGFEGEYKRLITFSEAPVFDVPHGSGRLRALSQIDSVLDLAR----- 58

Db 4 SAIGFEGYKRLVTFEPGLDTCQGLRALAKSQIDELQPAECTIVSSLSNDQLDS 63
 Qy 59 -----KIVIKTCGTTKLLTIPRIELEABELSMPLAAVKYSGRTFFPGAQP 105
 Db 64 YVLSSESLFFIPYKIVIKTCGTTKLLSIEPLRLAGELSLDKAVYTRGSLFCPGQP 123
 Qy 106 AHRSESEVAVLNRYFGGLKSGGNAYVIGDAARPGOKWHIYVATEYPEQPMVN---LEM 162
 Db 124 FPHRNSEEVSLDGHFAKGLGSLVAYLMGDDDET-KKHVYVYSSANSNNKNNVYVLEM 182
 Qy 163 CMTGLDTPKASVFFKTNADGNITCAKEMTKLSGISEIIPMEICDFDFPCGYSMAIHG 222
 Db 183 CMTGLDKDASVYK-----NESSAGSMTDNGIRKILPQSOICDFEFPCGYSMSIEG 238
 Qy 223 SAPSTIHTVPEDGFSYASVEVMGLDATALSYGDLVKRVLCGCPGSPFSVAV---TIFGGRG 280
 Db 239 DAISTIHVTPEDGFSYASVEAVGYDFTMDLSHLVSKVLCFCFKPQFSVAHVSTV---AQ 295
 Qy 281 QAGTWGKELGAEAYDCNNMVEQEL-PGGGILIIYQSF-----CAEEDAVASSPKSVLRCP 333
 Db 296 KSYDGLSLVDLDYGGCKESTWESLGEERGTVMYQRFKLGRYC-----GSPRSTLKCE 348
 Qy 334 DGENAAPFAKDCK 346
 Db 349 WSSNSCCNSEDEK 361

RESULT 13
 T10750
 probable adenosylmethionine decarboxylase (EC 4.1.1.50) - leaf mustard
 C;Species: Brassica juncea (leaf mustard)
 C;Date: 16-Jul-1999 #sequence,revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10750
 R;Lee, T.; Liu, J.J.; Pua, E.C.
 submitted to the EMBL Data Library, December 1996
 A;Reference number: Z17116
 A;Accession: T10750
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-369 <LEE>
 A;Cross-references: UNIPROT:O49972; EMBL:U80916; NID:G262405; PID:G2662406
 C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
 C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
 F;69/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 39.2%; Score 751; DB 2; Length 369;
 Best Local Similarity 46.1%; Pred. No. 1.6e-54;
 Matches 167; Conservative 48; Mismatches 91; Indels 56; Gaps 9;
 Qy 13 SAIGFEGYKRLVTFEPGLDTCQGLRALAKSQIDSVLDLAR----- 58
 Db 4 SAIGFEGYKRLVTFEPGLDTCQGLRALAKSQIDSVLDLAR----- 63
 Qy 59 -----KIVIKTCGTTKLLTIPRIELEABELSMPLAAVKYSGRTFFPGAQP 105
 Db 64 YVLSSESLFFIPYKIVIKTCGTTKLLSIEPLRLAGELSLDKAVYTRGSLFCPGQP 123
 Qy 106 AHRSESEVAVLNRYFGGLKSGGNAYVIGDAARPGOKWHIYVATEYPEQPMVN----- 159
 Db 124 FPHRNSEEVSLDGHFAKGLGSLVAYLMGDDDET-KKHVYVYSSANSNNKNNVY 182
 Qy 160 -LEMCTGLDTPKASVFFKTNADGNITCAKEMTKLSGISEIIPMEICDFDFPCGYSMN 218
 Db 183 TLEMCTGLDTPKASVFFKTNADGNITCAKEMTKLSGISEIIPMEICDFDFPCGYSMN 238
 Qy 219 AHRSESEVAVLNRYFGGLKSGGNAYVIGDAARPGOKWHIYVATEYPEQPMVN----- 278
 Db 239 SVEGDALSTIHTVPEDGFSYASVEAVGYDFTMDLSHLVSKVLCFCFKPQFSVAHVSSVA 298
 Qy 279 RQAGTWGKELGAEAYDCNNMVEQELPG---GGILIIYQSF-----CAEEDAVASSPKSVL 330
 Db 299 QKSYDS-GLSVLDLEDYGRE-TTIELLGEERGTVMYQSFKLGRYC-----GSPRSTL 349

Qy 331 RC 332
 Db 350 KC 351
 RESULT 14
 T22361
 adenosylmethionine decarboxylase (EC 4.1.1.50) precursor [validated] - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence,revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T22361; T27363; T43626; T43521
 R;White, S.
 submitted to the EMBL Data Library, September 1997
 A;Reference number: Z19553
 A;Accession: T22361
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-368 <WIL>
 A;Cross-references: UNIPROT:O02655; EMBL:Z99171; PIDN:CAA19560.1; GSPDB:GN00019; CESP:F47G4.7
 A;Experimental source: clone F47G4
 R;McLay, K.
 submitted to the EMBL Data Library, June 1998
 A;Reference number: Z20356
 A;Accession: T27363
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-368 <W12>
 A;Cross-references: EMBL:AL023853; PIDN:CAA19560.1; GSPDB:GN00019; CESP:F47G4.7
 A;Experimental source: clone Y71A12C
 R;Da'dara, A.A.; Walter, R.D.
 Biochem. J. 336, 545-550, 1998
 A;Title: Molecular and biochemical characterization of S-adenosylmethionine decarboxylase
 living nematode Caenorhabditis elegans, living nematode Caenorhabditis elegans.
 A;Reference number: Z22535; MUID:99059682; PMID:9841864
 A;Accession: T43626
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-368 <DAD>
 A;Cross-references: EMBL:Y12499; PIDN:CAA73101.1
 A;Accession: T43521
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-368 <DAD>
 A;Cross-references: EMBL:Y12500; PIDN:CAA73102.1
 C;Genetics:

A;Gene: samdc; F47G4.7
 A;Map position: 1
 A;Introns: 221/3; 294/2; 337/3
 C;Function:
 A;Description: EC 4.1.1.50 [validated, MUID:99059682]
 C;Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
 C;Keywords: blocked amino end; carbon-carbon lyase; carboxy-lyase
 F;83/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 19.7%; Score 377.5; DB 2; Length 368;
 Best Local Similarity 32.3%; Pred. No. 1.5e-23;
 Matches 108; Conservative 57; Mismatches 92; Indels 77; Gaps 16;
 Qy 17 FEGYKRLVTFEPGLDTCQGLRALAKSQIDSVLDLAR----- 58
 Db 25 FEGAKLLELWFCSS---TQNETRSLRITPREIDAMLDIARCKILKSHNESIDSVLS 81
 Qy 59 -----KIVIKTCGTTKLLTIPRIELEABELS-MPLAAVKYSGRTFFPGAQP 107
 Db 82 ESSLFISDNRNVLKTCGTTLLAALPVMQAGAYAGLDQVQSVYYSRKNFLPDLQPSL 141
 Qy 108 HRSFSEVAVLNRYFGGLKSGGNAYVIGDAARPGOKWHIY---YATEYP---EOPMVNLEM 162
 Db 142 HKNFDAEYVLOSFF---VDGHAYCIGSLKQ---DRWLYTFHREVEFFPAHKQPDHTEI 195
 Qy 163 CMTGLDTPKASVFFKTNADGNITCAKEMTKLSGISEIIPMEICDFDFPCGYSMN 220

Db 196 LMSDLDEVLHKTQYAVDGNDFMR-----AGIDKIIIPAGADVHDELDFPCGYSMNAY 250
Qy 221 HGSA--PSTIHVTPEDGFSVASYEVWGLDATALSYGLV-----KRVLCGFGPSEBSVA 272
Db 251 MNDDQVATHVTPKAFSPASE-----TNQDLVCLYSQTRKVLQCFRPNK--IL 299
Qy 273 VTIFGGRGQAGTWGKELGAEAYDCNNMVEQLPG 306
Db 300 MTFVA--NDISEKGKDAQQLWD-----RELPG 325

RESULT 15
DCHYDM
adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S22358; S19871
R;Tekwani, B.L.; Stanley, B.A.; Pegg, A.E.
Biochim. Biophys. Acta 1130, 221-223, 1992
A:Title: Nucleotide sequence of hamster S-adenosylmethionine decarboxylase cDNA.
A:Reference number: S22358; MUID:92223099; PMID:1562599
A:Accession: S22358
A:Molecule type: mRNA
A:Residues: 1-334 <TEK>
A:Cross-references: UNIPROT:P28918; EMBL:X63861; NID:G55521; PIDN:CAA45343.1; PID:G55522
A:Experimental source: liver of Syrian golden hamster
A:Note: the authors translated the codon ACA for residue 221 as Leu and AAG for residue 222 as Lys. The proenzyme is cleaved after translation into an alpha chain and a beta chain. The proenzyme is cleaved after translation into an alpha chain and a beta chain. The proenzyme is cleaved after translation into an alpha chain and a beta chain.
C:Comment: The proenzyme is cleaved after translation into an alpha chain and a beta chain. The proenzyme is cleaved after translation into an alpha chain and a beta chain. The proenzyme is cleaved after translation into an alpha chain and a beta chain.
C:Superfamily: S-adenosylmethionine decarboxylase, eukaryotic type
F:1-67/Domain: alpha chain #status predicted <CHA>
F:68-334/Product: adenosylmethionine decarboxylase #status predicted <MAT>
F:68-334/Domain: beta chain #status predicted <CHB>
F:68/Modified site: pyruvic acid (Ser) (in mature form) #status predicted

Query Match 18.8%; Score 359.5; DB 1; Length 334;
Best Local Similarity 33.6%; Pred. No. 4e-22;
Matches 99; Conservative 45; Mismatches 100; Indels 51; Gaps 12;

Qy 17 FEGYEKRLTTPSEAPVFPVDPHGSLRALRSQID-----SVLDLA----- 57
Db 7 FEGTEKLLVWFPSRQSDASQSGSGLRTIPRSEWDLKDVQCIIISVTKTQKQAYVLS 66
Qy 58 -----RKIVIKTCGTTKLLTIPRILELAEELS--MPLAAVKYSRGTFIPRGAQAP 107
Db 67 ESSMFVSKRRFIKTKCTTLLKALVPLKLARDYSGFDSIQSFYFYSRKNFMKPSHQYP 126
Qy 108 HRSFSEBVAVLNRYFGGLKSGGNAYVIGDAAPGQKWHIYYATEYEPQPMVN-----LEM 162
Db 127 HRNFQEEIEFLNAIF----PNGAAYCMG--RMNSDCWYL-YTLDFPESRVINQPDQTL 179
Qy 163 CMTGLDTKASVFKFNADGNTTCAKEMTKLGISETIPEMEICDFDFPCGYSMNAIHG 222
Db 180 LMSELDPAVMDQFYM--KDGVT--AKDVTRESGIRDLIPGSVIDATLFPNCGYSMNGMKS 235
Qy 223 -SAFSTIHVTPEDGFSVASYEVWGLDATALSYGLVLCRCPCPSEBSVAVTIF 276
Db 236 DGTWTYTHITPEPEFSYVSPET---NLQSYYDILIRKVVVEFKPGKF--VTTLF 285

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:40:28 ; Search time 75.8763 Seconds
(without alignments)
1620.151 Million cell updates/sec

Title: US-10-732-923-407

Perfect score: 1914

Sequence: 1 MAVLSAAGAPPAISAIGFEGY.....NLVCLFEKDAIBEKQGLVDE 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1853	96.8	366	15	US-10-310-154-457
2	1746.5	91.2	397	16	Sequence 457, App
3	1726	90.2	400	15	Sequence 47033, A
4	1538	80.4	450	16	Sequence 458, App
5	1538	80.4	466	16	Sequence 147033, A
6	1458	76.2	395	16	Sequence 147475, A
7	1458	76.2	554	16	Sequence 142922, A
8	1439.5	75.2	305	15	Sequence 142921, A
9	1393	72.8	398	16	Sequence 39365, A
10	1366.5	71.4	289	15	Sequence 46359, A
11	1365.5	71.3	416	15	Sequence 56960, A
12	1365.5	71.3	416	15	Sequence 57997, A
13	1359.5	71.0	422	15	Sequence 67343, A
					Sequence 36776, A

14	1302.5	68.1	276	15	US-10-425-114-69727	Sequence 69727, A
15	1244	65.0	392	16	US-10-437-963-128930	Sequence 128930, A
16	1218.5	63.7	395	16	US-10-767-701-46141	Sequence 46141, A
17	842.5	44.0	187	15	US-10-425-114-57416	Sequence 57416, A
18	829	43.3	355	15	US-10-424-599-249854	Sequence 249854, A
19	829	43.3	355	15	US-10-424-599-249859	Sequence 249859, A
20	829	43.3	356	15	US-10-425-114-46255	Sequence 46255, A
21	829	43.3	356	15	US-10-425-114-46648	Sequence 46648, A
22	809	42.3	355	15	US-10-424-599-249855	Sequence 249855, A
23	809	42.3	360	15	US-10-425-114-43048	Sequence 43048, A
24	809	42.3	360	15	US-10-425-114-4323	Sequence 46323, A
25	809	42.3	360	15	US-10-425-114-47297	Sequence 47297, A
26	802	41.9	363	14	US-10-380-913-4	Sequence 4, Appl
27	799.5	41.8	181	15	US-10-425-114-57901	Sequence 57901, A
28	778.5	40.7	173	15	US-10-425-114-56901	Sequence 56901, A
29	768	40.1	361	15	US-10-424-599-205003	Sequence 205003, A
30	751	39.2	331	15	US-10-425-114-71868	Sequence 71868, A
31	686	35.8	203	15	US-10-425-114-58490	Sequence 58490, A
32	676.5	35.3	156	15	US-10-425-114-47572	Sequence 47572, A
33	546.5	28.6	224	15	US-10-424-599-205002	Sequence 205002, A
34	468	24.5	359	16	US-10-437-963-166485	Sequence 166485, A
35	456.5	23.9	113	15	US-10-425-114-56995	Sequence 56995, A
36	439.5	23.0	216	15	US-10-425-114-45581	Sequence 45581, A
37	377.5	19.7	368	15	US-10-369-493-5296	Sequence 5296, Ap
38	377.5	19.7	368	15	US-10-369-493-5297	Sequence 5297, Ap
39	360.5	18.8	348	9	US-09-925-300-1167	Sequence 1167, Ap
40	356.5	18.6	334	15	US-10-341-434-12	Sequence 12, Appl
41	356.5	18.6	334	15	US-10-341-434-20	Sequence 20, Appl
42	356.5	18.6	334	15	US-10-341-434-127	Sequence 127, App
43	356.5	18.6	334	17	US-10-753-267-50	Sequence 50, Appl
44	346	18.1	369	15	US-10-369-493-2553	Sequence 2553, Ap
45	334	17.5	478	15	US-10-436-327-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-10-310-154-457
; Sequence 457, Application US/10310154
; Publication No. US2003023670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.

```

; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_367.pep
US-10-767-701-47033

Query Match      91.2%; Score 1746.5; DB 16; Length 397;
Best Local Similarity 85.9%; Pred. No. 1.5e-175;
Matches 341; Conservative 8; Mismatches 19; Indels 29; Gaps 2;

Oy 1 MAVLSAAGAPPASATGFGYKRLITFSEAPVFDPHGSLRALSRSQDSVLDLAR-- 58
Db 1 MAVLSAADAPPVSAITGFGYKRLITFSEAPVFDPHGSLRALSRSQDSVLDLARCT 60
Oy 59 -----KIVIKTCGTTKLLITIPRIELAEELSMPLAAVKY 93
Db 61 IVSELSNCKDFSYVLSSESLFIYPIKIVIKTCGTTKLLITIPRIELAEELSMPLAAVKY 120
Oy 94 SRGTTFPGAQAPAPHRSPFSEVAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYATEYP 153
Db 121 SRGTTFPGAQAPAPHRSPFSEVAVLNRYFGGLKSGGNAYVIGDAPRPGQKWHIYATEYP 180
Oy 154 EOPVYNLEMCMTGLDTKKASVFEKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 213
Db 181 EOPVYNLEMCMTGLDTKKASVFEKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 240
Oy 214 GYSMNAIHGSAFSTIHTVTPEDGFSYASVEVMGLDATALSYGDLVKRVLGFCGPFSEFSVAV 273
Db 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASVEVMGFDATALSYGDLVKRVLRCFGLPFSVAV 300
Oy 274 TIFGGRGAGTWGKELGAEAYDCNNMVQEQLPGGGIILYQSFCFAEADAVASSPKSVLRCP 333
Db 301 TIFGGRGAGTWGKELGAEAYDCNNMVQEQLPGGGIILYQSFCFAEADAVATSPKSVLHCF 360
Oy 334 DGENA--APFAKCKLANLVCLLEEKDAIEEKDGVLE 368
Db 361 EGVNENAPPVKRDKLANLLCWEEVDAMEEKDGVLE 397

RESULT 3
US-10-310-154-458
; Sequence 458, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Ameeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupall, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
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; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shishieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A.
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.

; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manchikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Tennesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 457
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Zea mays
US-10-310-154-457

Query Match      96.8%; Score 1853; DB 15; Length 366;
Best Local Similarity 100.0%; Pred. No. 7.1e-187;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MAVLSAAGAPPASATGFGYKRLITFSEAPVFDPHGSLRALSRSQDSVLDLARKI 60
Db 1 MAVLSAAGAPPASATGFGYKRLITFSEAPVFDPHGSLRALSRSQDSVLDLARKI 60
Oy 61 VIKTCGTTKLLITIPRIELAEELSMPLAAVKYSGRTTFPGAQAPAPHRSPFSEVAVLN 120
Db 61 VIKTCGTTKLLITIPRIELAEELSMPLAAVKYSGRTTFPGAQAPAPHRSPFSEVAVLN 120
Oy 121 YFGGLKSGGNNAVIGDAARPGQKWHIYATYBPQPMVYNLEMCMTGLDTKKASVFEKTN 180
Db 121 YFGGLKSGGNNAVIGDAARPGQKWHIYATYBPQPMVYNLEMCMTGLDTKKASVFEKTN 180
Oy 181 DGNNTCAKEMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAFSTIHTVTPEDGFSYAS 240
Db 181 DGNNTCAKEMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAFSTIHTVTPEDGFSYAS 240
Oy 241 YEVWGLDATALSYGDLVKRVLGFCGPFSEFSVAVTIFGGRGAGTWGKELGAEAYDCNNMV 300
Db 241 YEVWGLDATALSYGDLVKRVLGFCGPFSEFSVAVTIFGGRGAGTWGKELGAEAYDCNNMV 300
Oy 301 EQELPGGGIILYQSFCFAEADAVASSPKSVLRFCFDGNAAPFAKCKLANLVCLLEE 355
Db 301 EQELPGGGIILYQSFCFAEADAVASSPKSVLRFCFDGNAAPFAKCKLANLVCLLEE 355

RESULT 2
US-10-767-701-47033
; Sequence 47033, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 47033
; LENGTH: 397
; TYPE: PRT

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; LOCATION: (1)...(466)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_479C.1.pep
US-10-437-963-147475

Query Match      80.4%; Score 1538; DB 16; Length 466;
Best Local Similarity 77.0%; Pred. No. 2.2e-153;
Matches 308; Conservative 18; Mismatches 40; Indels 34; Gaps 5;

QY 1 MAVLSAAGAPPASAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLAR-- 58
Db 69 MGVLSAADPPVSAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLARCT 128
QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 93
Db 129 IVSELSNEVFD SYVLSSESLFVYPIKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 188
QY 94 SRTGTFIPGAOPAPHRFSFSEVAVLNRYFGGLSGGNAYVIGDAARPGQKWHIYYATEYP 153
Db 189 SRGMFIPPSAOPAPHRFSFSEVAVLNRYFGHLKSGGNAYVIGDPAKPGQKWHIYYATQHP 248
QY 154 EQPMVNLMECMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 213
Db 249 EQPMVNLMECMTGLDKKASVFFKTSADGHTTCAKEMTKLSGSDIIPEMEICDFDEPC 308
QY 214 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGDLNATLSYGDILVKRVLCFGSPSEFSVAV 273
Db 309 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGDLNATLSYGDILVKRVLCFGSPSEFSVAV 368
QY 274 TIFGGGOAGTGWCKELGAEAYDCNNMVQELPGGGLIYQSFCAED--AVASSPKSVLR 331
Db 369 TIFGGHGHAGTGWAKELNADAYKCNMVQELPGCGLLIYQSFDTATEDVPVAVGSPKSVLH 428
QY 332 CFPGCE--NNAAPFAKCKLANLVCLBEXDAIEEKQGVLDE 368
Db 429 CFEAENWNPAP-VKSGKLGNLPLPWGE-DALENDGWFDE 466

RESULT 6
US-10-437-963-142922
; Sequence 142922, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142922
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43881C.1.pep
US-10-437-963-142922

Query Match      76.2%; Score 1458; DB 16; Length 395;
Best Local Similarity 73.0%; Pred. No. 4.9e-145;
Matches 286; Conservative 25; Mismatches 47; Indels 34; Gaps 3;

QY 1 MAVLSAAGAPPASAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLAR-- 58
Db 1 MAVLSVADSPVSAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLARCT 131
QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 93
Db 132 IVSELSNEVFD SYVLSSESLFVYPIKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 191
QY 94 SRTGTFIPGAOPAPHRFSFSEVAVLNRYFGGLSGGNAYVIGDAARPGQKWHIYYATEYP 153
Db 192 SRTGTFIPGAOPAPHRFSFSEVAVLNRYFGGLSGGNAYVIGDPAKPGQKWHIYYATQHP 251
QY 154 EQPMVNLMECMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 213
Db 1 MAVLSVADSPVSAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLARCT 60

; LOCATION: (1)...(466)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_479C.1.pep
US-10-437-963-147475

Query Match      80.4%; Score 1538; DB 16; Length 466;
Best Local Similarity 77.0%; Pred. No. 2.2e-153;
Matches 308; Conservative 18; Mismatches 40; Indels 34; Gaps 5;

QY 1 MAVLSAAGAPPASAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLAR-- 58
Db 69 MGVLSAADPPVSAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLARCT 128
QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 93
Db 129 IVSELSNEVFD SYVLSSESLFVYPIKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 188
QY 94 SRTGTFIPGAOPAPHRFSFSEVAVLNRYFGGLSGGNAYVIGDAARPGQKWHIYYATEYP 153
Db 189 SRGMFIPPSAOPAPHRFSFSEVAVLNRYFGHLKSGGNAYVIGDPAKPGQKWHIYYATQHP 248
QY 154 EQPMVNLMECMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 213
Db 249 EQPMVNLMECMTGLDKKASVFFKTSADGHTTCAKEMTKLSGSDIIPEMEICDFDEPC 308
QY 214 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGDLNATLSYGDILVKRVLCFGSPSEFSVAV 273
Db 309 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVMGDLNATLSYGDILVKRVLCFGSPSEFSVAV 368
QY 274 TIFGGGOAGTGWCKELGAEAYDCNNMVQELPGGGLIYQSFCAED--AVASSPKSVLR 331
Db 369 TIFGGHGHAGTGWAKELNADAYKCNMVQELPGCGLLIYQSFDTATEDVPVAVGSPKSVLH 428
QY 332 CFPGCE--NNAAPFAKCKLANLVCLBEXDAIEEKQGVLDE 368
Db 429 CFEAENWNPAP-VKSGKLGNLPLPWGE-DALENDGWFDE 466

RESULT 7
US-10-437-963-142921
; Sequence 142921, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142921
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43880C.1.pep
US-10-437-963-142921

Query Match      76.2%; Score 1458; DB 16; Length 554;
Best Local Similarity 73.0%; Pred. No. 8.2e-145;
Matches 286; Conservative 25; Mismatches 47; Indels 34; Gaps 3;

QY 1 MAVLSAAGAPPASAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLAR-- 58
Db 72 MAVLSVADSPVSAI GFE GYKLEITFS EAPVFD PHGSLRALSRQSDSVLDLARCT 131
QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 93
Db 132 IVSELSNEVFD SYVLSSESLFVYPIKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 191
QY 94 SRTGTFIPGAOPAPHRFSFSEVAVLNRYFGGLSGGNAYVIGDAARPGQKWHIYYATEYP 153
Db 192 SRTGTFIPGAOPAPHRFSFSEVAVLNRYFGGLSGGNAYVIGDPAKPGQKWHIYYATQHP 251
QY 154 EQPMVNLMECMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDEPC 213
Db 252 EQPMVNLMECMTGLDKKASVFFKTSADGHTTCAKEMTKLSGSDIIPEMEICDFDEPC 311
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QY 214 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLGCGFSPSEFSVAV 273
Db 312 GYSNNAIHGSAFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLGCGFSPSEFSVAV 371
QY 274 TIFGGRQAGTGWKELGAEAYDCNNMVEQLPGGILLIYQSFCAEDAVASSPKSVLRCP 333
Db 372 TIFGGRNAGTGWKGLDVGAYSCNNMVEQLPGGILLIYQSFATATATGSRVSLHCF 431
QY 334 DGENAAPPFAKCKLANIIVCL-EXDAIEEKDG 364
Db 432 ADENTE-----KAGKWEALYWEDDAVEEDG 457

RESULT 8
US-10-425-114-39365
; Sequence 39365, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39365
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700074853_FLI.pep
US-10-425-114-39365

Query Match 75.2%; Score 1439.5; DB 15; Length 305;
Best Local Similarity 90.2%; Pred. No. 3e-143;
Matches 275; Conservative 7; Mismatches 18; Indels 5; Gaps 2;

QY 69 KLLTTPRIELABELSMPAAVKYSGTTFPGAQAPAPHRSPSEEVAVLNRYFGGLKSG 128
Db 1 KLLTTPRIELABELSMPAAVKYSGTTFPGAQAPAPHRSPSEEVAVLNRYFGGLKSG 60

QY 129 GNAYVIGDAPAPGQKWHIYATYEPQPMVNLEMCMTGLDTKKASVFFKTNADGNTTCAK 188
Db 61 GNAYVIGDAPAPGQKWHIYATYEPQPMVNLEMCMTGLDTKKASVFFKTNADGNTTCAK 120

QY 189 EMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAFSTIHTVPEDGFSYASYEVNGLDA 248
Db 121 EMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAFSTIHTVPEDGFSYASYEVNGLDA 180

QY 249 TALSYGDLVKRVLGCGFSPSEFSVAVTIFGGRQAGTGWKELGAEAYDCNNMVEQLPGGG 308
Db 181 TALSYGDLVKRVLGCGFSPSEFSVAVTIFGGRHAGTGWKALGAEVYDCNNMVEQLPGGG 240

QY 309 ILIYQSFCAEDAVASSPKSVLRCPDGENA----APPFAKCKLANIIVCL-EEKDAIEEKD 363
Db 241 LLVYQSFCAEDAVATSPKSVFHFCDGENVESAPPPMKDYKLANILLCWEEDAMEKA 300

QY 364 GVLDE 368
Db 301 GVLDE 305

RESULT 9
US-10-767-701-46359
; Sequence 46359, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46359
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1511_1.pep
US-10-767-701-46359

Query Match 72.8%; Score 1393; DB 16; Length 398;
Best Local Similarity 70.4%; Pred. No. 3.8e-138;
Matches 276; Conservative 35; Mismatches 49; Indels 32; Gaps 4;

QY 1 MAVL--SAAGAPPASAIPEGYEKRLIETSEAPVFDPHGSLRLALSRQIDSVLDLAR 58
Db 1 MAVLQVAAAAPPVSAIGFEGYEKRLIETSEAPVFDPNRGLRLALSRQIDSVLDLAR 60

QY 59 -----KIVIKTCGTTKLLLTTPRIELEAEELSMPAAV 91
Db 61 CTIVSLSNBEDFDSYVLSASSLFVYPYKMWIKTCGTTKLLLTTPRIELEAEELSMPAAV 120

QY 92 KYSRGTFIPGAQAPAPHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPCQKWHIYATE 151
Db 121 KYSRGTFIPGAQAPAPHRSPSEEVAVLNRYFGGLKSGNAYVIGDAARPCQKWHIYATE 180

QY 152 YPEQPMVNLEMCMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFE 211
Db 181 HPEEPVVTLEMCMTGLDTKKASVFFKTSADGYTSCAKEMTKLSGISIIPEMEICDFDFE 240

QY 212 PCGYSMNAIHGSAFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLGCGFSPSEFSV 271
Db 241 PCGYSMNAIHGSAFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLGCGFSPSEFSV 300

QY 272 AVTIFGGRQAGTGWKELGAEAYDCNNMVEQLPGGILLIYQSFCAEDAVASSPKSVLR 331
Db 301 AVTIFGGRNAGTGWKELGAEAYDCNNMVEQLPGGILLIYQSFATATGSRVSLH 360

QY 332 CPDGENAAPPFAKCKLANIIVCL-EXDAIEEKD 363
Db 361 DFAGDIVKP--GDSGEADGFCW-EADAVDESE 389

RESULT 10
US-10-425-114-56960
; Sequence 56960, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56960
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17089E06_FLI.pep
US-10-425-114-56960


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; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36776
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-020-E2_FLI.pbp
US-10-425-114-36776

Query Match 71.0%; Score 1359.5; DB 15; Length 422;
Best Local Similarity 67.4%; Pred. No. 1.4e-134;
Matches 269; Conservative 33; Mismatches 48; Indels 49; Gaps 4;

QY 1 MAVL--SAAGAPASAIAGFEGYKRLITFPSEAPVFDVPHGSLRALRSQIDSVDLDLAR 58
DB 28 MAVLVQAAAAPPVSVVIGFEGFKRLISFSEAPVLADPSGRGLRALSRAQIDSVDLDLAR 87
QY 59 -----KIVIKTCGTTKLLTTPRILELAELSMPLAAV 91
DB 88 CTIVSELSNEDFDSYVLSSESLFVYPYKIVIKTCGTTKLLTTPRILELAELSMPLAAV 147
QY 92 KYSGCTFIFPGAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPCOKWHIYYATE 151
DB 148 KYSGCTFIFPEAOPSPHKNFADVAFNRFPGGLKSGGNAYVIGDSAKPGQKWHIYYAE 207
QY 152 YPQPQVNVLEMCMGTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDPDFE 211
DB 208 HPEPVVTVLEMCMGTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDPDFE 267
QY 212 PCYSNNAIHGSAFSTIHTVTPEDGFSYASVYVNGLDATALSVDLVKRVLCFGPSEFSV 271
DB 268 PCYSNNAHVGPALSTIHTVTPEDGFSYASVYVNGFNPSPSYGDLVKRVLCFGPTEFSV 327
QY 272 AVTIFGCGOAGTWGKELGAEYDCNNMVEQELPGCGILLIYQSFCAEDAVASSPKSVLR 331
DB 328 AVTIFGDRNNAKTGKLDAAEYACSNMVEQVLPFGGLLIYQSFVTAETTHGSPRSVLH 387
QY 332 CPGD-----ENAAFPKDKLANLVCLLEEXDAIEBKD 363
DB 388 DFAGDIVKRNSESDAPW-----EADAVDESE 413

RESULT 14
US-10-425-114-69727
; Sequence 69727, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69727
; LENGTH: 276

; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17199H04_FLI.pbp
US-10-425-114-69727

Query Match 68.1%; Score 1302.5; DB 15; Length 276;
Best Local Similarity 89.1%; Pred. No. 8.2e-129;
Matches 246; Conservative 7; Mismatches 18; Indels 5; Gaps 2;

QY 98 FIFPGAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPCOKWHIYYATEYEQPM 157
DB 1 FIFPGAPAPHRSESEAVLNRYFGLKSGGNAYVIGDPAIPGQKWHIYYATEYEQPM 60
QY 158 VNLEMCMTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPGCGYSM 217
DB 61 VNLEMCMTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPGCGYSM 120
QY 218 NAIHGSFAFSTIHTVTPEDGFSYASVYVNGLDATALSVDLVKRVLCFGPSEFSVAVTIFG 277
DB 121 NAIHGSFAFSTIHTVTPEDGFSYASVYVNGLDATALSVDLVKRVLCFGPSEFSVAVTIFG 180
QY 278 GRGOAGTWGKELGAEYDCNNMVEQELPGCGILLIYQSFCAEDAVASSPKSVLCRFDGEN 337
DB 181 GRGHAGTWGKALGAEYDCNNMVEQELPGCGILLIYQSFCAEDAVATSPKSVFHCFDGEN 240
QY 338 A----APPFAKDKLANLVCL-EXXDAIEBKDGVLDE 368
DB 241 VESAPPPMKDYKLANLLCWEEDANDEKAGVLDE 276

RESULT 15
US-10-437-963-128930
; Sequence 128930, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128930
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31236C.1.pbp
US-10-437-963-128930

Query Match 65.0%; Score 1244; DB 16; Length 392;
Best Local Similarity 62.6%; Pred. No. 2.1e-122;
Matches 244; Conservative 48; Mismatches 68; Indels 30; Gaps 3;

QY 1 MAVLSAAGAPPASAIAGFEGYKRLITFPSEAPVFDVPHGSLRALRSQIDSVDLDLAR-- 58
DB 3 MSLADWSGAPASAIAGFEGYKRLITLSDAPVFDVPCGRGLRALREQIDSLDLAKCT 62
QY 59 -----KIVIKTCGTTKLLTTPRILELAELSMPLAAVKY 93
DB 63 IVSHLSNKHFDSDYVLSSESLFVYPYKVKVLTCTGTTKLLTTPRILELAELSLPVLVKY 122
QY 94 SRGTFFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPCOKWHIYYATEYP 153
DB 123 SRGMFIFPGAQSPHRSFLEEVSVLNSFFGGLKSGGNAYVIGDAFPKPKKWHIYYATEEP 182
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; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36776
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-020-E2_FLI.pbp
US-10-425-114-36776

Query Match 71.0%; Score 1359.5; DB 15; Length 422;
Best Local Similarity 67.4%; Pred. No. 1.4e-134;
Matches 269; Conservative 33; Mismatches 48; Indels 49; Gaps 4;

QY 1 MAVL--SAAGAPASAIAGFEGYKRLITFPSEAPVFDVPHGSLRALRSQIDSVDLDLAR 58
DB 28 MAVLVQAAAAPPVSVVIGFEGFKRLISFSEAPVLADPSGRGLRALSRAQIDSVDLDLAR 87
QY 59 -----KIVIKTCGTTKLLTTPRILELAELSMPLAAV 91
DB 88 CTIVSELSNEDFDSYVLSSESLFVYPYKIVIKTCGTTKLLTTPRILELAELSMPLAAV 147
QY 92 KYSGCTFIFPGAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPCOKWHIYYATE 151
DB 148 KYSGCTFIFPEAOPSPHKNFADVAFNRFPGGLKSGGNAYVIGDSAKPGQKWHIYYAE 207
QY 152 YPQPQVNVLEMCMGTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDPDFE 211
DB 208 HPEPVVTVLEMCMGTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDPDFE 267
QY 212 PCYSNNAIHGSAFSTIHTVTPEDGFSYASVYVNGLDATALSVDLVKRVLCFGPSEFSV 271
DB 268 PCYSNNAHVGPALSTIHTVTPEDGFSYASVYVNGFNPSPSYGDLVKRVLCFGPTEFSV 327
QY 272 AVTIFGCGOAGTWGKELGAEYDCNNMVEQELPGCGILLIYQSFCAEDAVASSPKSVLR 331
DB 328 AVTIFGDRNNAKTGKLDAAEYACSNMVEQVLPFGGLLIYQSFVTAETTHGSPRSVLH 387
QY 332 CPGD-----ENAAFPKDKLANLVCLLEEXDAIEBKD 363
DB 388 DFAGDIVKRNSESDAPW-----EADAVDESE 413

RESULT 14
US-10-425-114-69727
; Sequence 69727, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69727
; LENGTH: 276

; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17199H04_FLI.pbp
US-10-425-114-69727

Query Match 68.1%; Score 1302.5; DB 15; Length 276;
Best Local Similarity 89.1%; Pred. No. 8.2e-129;
Matches 246; Conservative 7; Mismatches 18; Indels 5; Gaps 2;

QY 98 FIFPGAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPCOKWHIYYATEYEQPM 157
DB 1 FIFPGAPAPHRSESEAVLNRYFGLKSGGNAYVIGDPAIPGQKWHIYYATEYEQPM 60
QY 158 VNLEMCMTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPGCGYSM 217
DB 61 VNLEMCMTGLDKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPGCGYSM 120
QY 218 NAIHGSFAFSTIHTVTPEDGFSYASVYVNGLDATALSVDLVKRVLCFGPSEFSVAVTIFG 277
DB 121 NAIHGSFAFSTIHTVTPEDGFSYASVYVNGLDATALSVDLVKRVLCFGPSEFSVAVTIFG 180
QY 278 GRGOAGTWGKELGAEYDCNNMVEQELPGCGILLIYQSFCAEDAVASSPKSVLCRFDGEN 337
DB 181 GRGHAGTWGKALGAEYDCNNMVEQELPGCGILLIYQSFCAEDAVATSPKSVFHCFDGEN 240
QY 338 A----APPFAKDKLANLVCL-EXXDAIEBKDGVLDE 368
DB 241 VESAPPPMKDYKLANLLCWEEDANDEKAGVLDE 276

RESULT 15
US-10-437-963-128930
; Sequence 128930, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128930
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31236C.1.pbp
US-10-437-963-128930

Query Match 65.0%; Score 1244; DB 16; Length 392;
Best Local Similarity 62.6%; Pred. No. 2.1e-122;
Matches 244; Conservative 48; Mismatches 68; Indels 30; Gaps 3;

QY 1 MAVLSAAGAPPASAIAGFEGYKRLITFPSEAPVFDVPHGSLRALRSQIDSVDLDLAR-- 58
DB 3 MSLADWSGAPASAIAGFEGYKRLITLSDAPVFDVPCGRGLRALREQIDSLDLAKCT 62
QY 59 -----KIVIKTCGTTKLLTTPRILELAELSMPLAAVKY 93
DB 63 IVSHLSNKHFDSDYVLSSESLFVYPYKVKVLTCTGTTKLLTTPRILELAELSLPVLVKY 122
QY 94 SRGTFFPGAQAPAPHRSESEAVLNRYFGLKSGGNAYVIGDAARPCOKWHIYYATEYP 153
DB 123 SRGMFIFPGAQSPHRSFLEEVSVLNSFFGGLKSGGNAYVIGDAFPKPKKWHIYYATEEP 182
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Qy	154	EQPWNLEMCMTGLDTKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFPC	213
Db	183	EQPWNLEMCMTGLDAKAEVFFKDSGSSAKEMTFSGISEIIPEMEICDFDFPC	242
Qy	214	GYSNNAIHGSAFSTIHVTPEDGFSYASYEVNGLDATALSYGDLVKRVLGCFGPSEFSVAV	273
Db	243	GYSNNGIYGPAVSTIHVTPPEGFSYASYEAMNFPSSLVYDDLIKKVLACFCPSDFSVAV	302
Qy	274	TIFGGRGQAGTWKELGAEAAYDCNNMVEQELPGGGLIYQSFCAAEADAVASSPKSVLRCF	333
Db	303	TIFGCHGFAKSWAKAEVDSYMCDDLVEQELPGGVLMYQSFTAVTPG-AVSPRSTLDGW	361
Qy	334	DGENAAPPFAKCKLANLVCLLEEXDATEEKD	363
Db	362	NSDGAENVAKSEMS--VCWEGEKAARKKD	389

Search completed: May 11, 2005, 22:57:57
Job time : 76.8763 secs

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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:39:42 ; Search time 24.3436 Seconds
(without alignments)
1128.461 Million cell updates/sec

Title: US-10-732-923-407
Perfect score: 1914
Sequence: 1 MAVLSAAGAPPASAIAGFEY.....NLVLEEXDAIBEKGVLD 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360.5	18.8	348	4	US-09-949-016-10038
2	356.5	18.6	334	4	US-09-917-254-54
3	331	17.3	424	4	US-09-248-796A-18169
4	97.5	5.1	350	4	US-09-302-540-11867
5	96.5	5.0	410	4	US-09-010-877-2
6	94.5	4.9	331	4	US-09-710-279-874
7	94.5	4.9	331	4	US-09-710-279-2244
8	94.5	4.9	342	3	US-09-134-001C-5198
9	94.5	4.9	634	4	US-09-248-796A-19513
10	89	4.6	308	3	US-09-189-060B-70
11	89	4.6	3546	4	US-09-679-279-13
12	86.5	4.5	535	1	US-08-008-688A-2
13	86.5	4.5	545	4	US-09-604-957-4
14	86.5	4.5	1430	3	US-09-008-172-2
15	86.5	4.5	1430	3	US-09-210-361-6
16	86.5	4.5	1430	4	US-09-740-274-6
17	86	4.5	532	4	US-09-252-991A-25188
18	85.5	4.5	270	2	US-08-773-368-1
19	85.5	4.5	270	3	US-09-199-887-1
20	85.5	4.5	1056	2	US-08-627-873-7
21	85	4.4	288	4	US-09-270-767-43786
22	85	4.4	332	4	US-09-252-991A-21222
23	85	4.4	755	5	PCT-US93-07923-3
24	85	4.4	759	5	PCT-US93-07923-2
25	85	4.4	766	1	US-08-230-491A-3
26	85	4.4	766	1	US-08-619-280A-3
27	85	4.4	766	2	US-08-940-391-3

28	85	4.4	766	3	US-09-794-236-1	Sequence 1, Appli
29	85	4.4	766	4	US-10-002-593-6	Sequence 6, Appli
30	85	4.4	766	4	US-09-949-016-6146	Sequence 6146, Ap
31	85	4.4	775	4	US-09-949-016-10450	Sequence 10450, A
32	84	4.4	450	2	US-08-861-464-2	Sequence 2, Appli
33	84	4.4	450	2	US-08-396-001-2	Sequence 2, Appli
34	84	4.4	450	3	US-09-323-433A-2	Sequence 2, Appli
35	84	4.4	450	4	US-09-826-752-2	Sequence 11561, A
36	84	4.4	898	4	US-09-902-540-11561	Sequence 197, App
37	83.5	4.4	285	3	US-09-095-855-197	Sequence 197, App
38	83.5	4.4	285	4	US-09-205-426-197	Sequence 3382, Ap
39	83.5	4.4	687	4	US-09-107-433-3382	Sequence 16119, A
40	83.5	4.4	1068	4	US-09-248-796A-16119	Sequence 1, Appli
41	83	4.3	305	2	US-08-795-475-1	Sequence 1, Appli
42	83	4.3	305	4	US-08-325-278B-1	Sequence 3, Appli
43	83	4.3	434	2	US-08-795-475-3	Sequence 3, Appli
44	83	4.3	434	4	US-08-325-278B-3	Sequence 1030, Ap
45	82.5	4.3	496	4	US-09-710-279-1030	

ALIGNMENTS

RESULT 1
US-09-949-016-10038
; Sequence 10038, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10038
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10038

Query Match	18.8%	Score	360.5;	DB	4;	Length	348;
Best Local Similarity	33.9%	Pred. No.	3.9e-32;				
Matches	100;	Conservative	44;	Mismatches	100;	Indels	51;
Gaps	12;						
QY	17	FEYKRLITSEAPVFDPHGSLRALSRSID	-----SVLDLA-----	57			
DB	21	FEGETLLEWFSRQPDANQSGDLRTIPRSEWILLKDVQCSIIISVTKDKQEAIVLS	80				
QY	58	-----RKIVTKGTGTLKLLITIPRIELAEELS--MPLAAVKYSRGTFIPFGAQPAP	107				
DB	81	ESSMFVKRRFLTKTCGTLILLKALVPLKLRDYSGFDSIQSFYSRKRNKMPKPSHQYCP	140				
QY	108	HRFSFSEAVLNRYFGGLKSGGNAYVIGDAARPGQKWHIYYATEYPE-----QPMVNLEM	162				
DB	141	HRNFQSEIEFLNAIF---PNGAAYCMG--RWNSDCMYL-YTLDFPESRVISQPDQLEI	193				
QY	163	CMTGLDTKASVFFKTNAGNTTCAKEMTKLSIISIIEMEICDFDFPCGYSMAIHG	222				
DB	194	LMSLDPVMDQFYM--KDGVT--AKDVTRESGIROLIFGSVIDATMFPNCGYSMAHGMKS	249				
QY	223	-SAFSTIHTVTPDEGFSYASVEVMGLDATALSYGLVKRVLGCGFSPSEFSVAVTIF	276				
DB	250	DGTWTIHTIHTPEPFSIVSFET---NLSQTSYDILLRKVVVEFKPKGF---VTTLF	299				

RESULT 2

US-09-917-254-54
; Sequence 54, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224 (JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-54

Query Match 18.6%; Score 356.5; DB 4; Length 334;
Best Local Similarity 33.6%; Pred. No. 1e-31;
Matches 99; Conservative 44; Mismatches 101; Indels 51; Gaps 12;
QY 17 FEGYKRLTFSEAPVFDPHGSGRLALRSQID-----SVLDLA----- 57
DB 7 FEGTEKLEVFQRQPDANQSGDLRTIPRSEWDILLKDVQCSIIISVTKTKDQOEAYVLS 66
QY 58 -----RKIVTKCTGTTKLLITIPRILELAELS--MPLAAVKYSRGTFIFPGAQAP 107
DB 67 ESSMFVSKRRFIKTKGTTLLKALVPLKLDYSGFDSIQSFYRKRKMFPSHQYP 126
QY 108 HRFSFBEAVLNRYFGKLSGKNAYVIGDARPGQKWHIYATEYPE-----QPMVNLEM 162
DB 127 HRNFQEBEFLNAIF---PNGAGYCMG--RMNSDCWYL-YTLDFPESRVISQPDQTL 179
QY 163 CMTGLDTKASVFFKTNADNTTCAKEMTKLSGISELIPMEICDFDFPCGYSMAIHG 222
DB 180 LMSELDPAVNDQPYM--KQGV--AKDVTRESGIRDLPGSVIDATMFPNPGYSMNGMS 235
QY 223 -SAFSTHVPEDGFSYASVEVMGLDATALSYGDLVKRVLGCGFSPSEFSVATIF 276
DB 236 DGYTWIHIHTEPESFVSFET---NLSQTSYDILLIRKVEVPKPKGF--VTILF 285

RESULT 3

US-09-248-796A-18169
; Sequence 18169, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18169
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18169

Query Match 17.3%; Score 331; DB 4; Length 424;
Best Local Similarity 29.9%; Pred. No. 1.3e-28;
Matches 100; Conservative 49; Mismatches 98; Indels 88; Gaps 13;
QY 13 SAIGFEGYKRLTTFSE-----APVFVDP-----HSGSLRALSQID---- 51

Db 61 SHAFEGPEKLEINWFYESKELSPINLRDIKFDPTWIEILNVHCEVLKSVSSNLCDAFL 120
QY 52 ----SVLDLARKIVIKTCGTTKLLITIPRILE-LAEEL-----SNPLAAVKYSRG 96
Db 121 SSSLFVFPKIKLTKGTTTLLACLDFETVNKELLQNEGLKATFQSKNIYQIFYSRR 180
QY 97 TIFPGAQAPHRSPSEYAVLNRYFGKLSGKNAYVIGDARPGQKWHIY----- 148
Db 181 SFMFPDRQIHVHGNWQEEVKLLNQYF-----NNGKSYIVGN-----NTNWHLYVGNKTKN 232
QY 149 ----ATEYPEQPMVN---LEMCMTGDLTKKASVFFKTNADGNTT-----CAKEMT 191
Db 233 PVASTTTTTTPVNDCTLEIIMTQLSLEASQOFTYTRKPGDTAIDSNHDLGDLQEIL 292
QY 192 KLSGISEII-----PEMEICD-FDFPCGYSMAIHGSAFSTHVTPEDFG 236
Db 293 KQTGLNELFKKQKPTMPGLSSSPIKEIHDFGFAFTCGFSSNSINESNYTTHVTPEPGW 352
QY 237 SYASVEVMGLDATALSYGDLVKRVLGCGFSPSEFSV 271
Db 353 SYASPETNMIG----DYKAIVDKINNVFQGPQPMV 383

RESULT 4

US-09-902-540-11867
; Sequence 11867, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11867
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11867

Query Match 5.1%; Score 97.5; DB 4; Length 350;
Best Local Similarity 20.8%; Pred. No. 0.042;
Matches 55; Conservative 30; Mismatches 111; Indels 69; Gaps 9;

QY 144 WHIYATEYPEQPMVNLEMCMTGDLTKKASVFFKTNADGNTTCAKEMTKLSGISELIP 203
Db 37 WHV--SNFYSQPIDLAAQLTWSGLSRAFFCNSGAANEALLKTRKVMKDRGTPERF 94
QY 204 EICDPDFPCGYSMAIHGSAFSTHVTPEDFGFSYASVEVMGLDATALSYGDLVKRVLG 263
Db 95 EVISFD-----SSFHRTLATVTATGOAKYQ-KGFPELPAGFTHVPFCDL-EAVRKA 144
QY 264 FGPSEFSVAVTIFGGRGQA-----GTWKELGAE 292
Db 145 VGPATAAILVEPIQEGGVRMAPLGLVLRALCDEHGLLLLVDEVTQGMGRGKPGF- 203
QY 293 AYDCNNVQEPL-----GGGILIYQSFCAAEDAVASSPKSVLRCFDGDNAPPAK 343
Db 204 -----MHGIVPDGISVAKALGNGLPIGAMLCKEELGASLTPTGHTSGTFGPNVAAAA- 256
QY 344 DCKLANLVCLXEEXDAJEEKDGVLD 368
Db 257 ----ANAV-----RILRRPGFLDE 272

RESULT 5

US-09-010-877-2

```
; Sequence 2, Application US/09010877B
; Patent No. 6444445
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Nikolich, Mikeljon
; APPLICANT: Hoover, David L.
; APPLICANT: Warren, Richard L.
; APPLICANT: Lindler, Luther E.
; APPLICANT: Hadfield, Ted L.
; APPLICANT: Boyle, Stephen M.
; APPLICANT: McQuiston, John R.
; APPLICANT: Schurig, Gerhard G.
; APPLICANT: Nammalwar Sriranganathan
; TITLE OF INVENTION: Live Vaccines Against Brucellosis
; FILE REFERENCE: Army-124
; CURRENT APPLICATION NUMBER: US/09/010,877B
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: NO. 6444445e
; EARLIER FILING DATE: NO. 6444445e
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PC-IBM compatible
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Brucella abortus
US-09-010-877-2

Query Match      5.0%; Score 96.5; DB 4; Length 410;
Best Local Similarity 24.0%; Pred. No. 0.072;
Matches 47; Conservative 28; Mismatches 82; Indels 39; Gaps 9;

QY 98 FIFGQAPAPRFSSEVAVLNRYFGLKSGGNAYVIGDAA---RPGQKWHIYYATEYPE 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 217 FLWP-TNPNAKHAKAFQALDIYGLKGIKTKIVGVSSVRMDPSHRQAKYEN---K 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 155 QPMVNLEMCMTGLDTKASVFF-----KTNADGNNTCAKEMTKL 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 273 AVYKSVREIVAGLDNLKSNVEFAGEVADKEYAEILLASACFFMHTLADNGTFAAVEAYM 332

QY 194 S--GISEIIPEMEICDFDFE-PCGYSMNAIH-----GSAFTIHVTPEDGFSYASYVMGL 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 333 GCPTLSNDYQPMRYINRFFIPMQY-FNARSVKEMASALKQMBETPIDVGLLPSRTL 391

QY 247 ---DATAISYGLDVLR 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 392 HSWENHASEYWDVIR 407

RESULT 6
US-09-710-279-874
; Sequence 874, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 874
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-874

Query Match      4.9%; Score 94.5; DB 4; Length 331;
Best Local Similarity 22.7%; Pred. No. 0.085;
Matches 45; Conservative 32; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLEMCMTGLDTKASVFFKTNADGNNTCA-----KEMT 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 59 FIQTNPQPFYFNKAMCVCGTGGDSNSP-----NISTTVAFVVASAGVPVIKHGNSIT 113

QY 192 KLSGISEIIPEMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGF-----SYAS 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 114 SHSGSTDVLHEMNIKTNKMEVEQQLN-LKGLAF-----ISATDSYPMMKLQSIKSIAT 168

QY 241 YEVMGLDATALSYGDLVKRVLGCGFSEF-SVAVTIFGGRGQAGTWGKEIGAE----AYD 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 PTIFNLIGLPLNPFKLTYYQVMGYVEASOLENIAQTL-----KDLGRKRAILIHG 217

QY 296 CNNMVEQELPGGGILIYQ 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 218 ANGMDEATLSGENI-IYE 234

RESULT 7
US-09-710-279-2244
; Sequence 2244, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2244
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-2244

Query Match      4.9%; Score 94.5; DB 4; Length 331;
Best Local Similarity 22.7%; Pred. No. 0.085;
Matches 45; Conservative 32; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLEMCMTGLDTKASVFFKTNADGNNTCA-----KEMT 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 59 FIQTNPQPFYFNKAMCVCGTGGDSNSP-----NISTTVAFVVASAGVPVIKHGNSIT 113

QY 192 KLSGISEIIPEMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGF-----SYAS 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 114 SHSGSTDVLHEMNIKTNKMEVEQQLN-LKGLAF-----ISATDSYPMMKLQSIKSIAT 168

QY 241 YEVMGLDATALSYGDLVKRVLGCGFSEF-SVAVTIFGGRGQAGTWGKEIGAE----AYD 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 PTIFNLIGLPLNPFKLTYYQVMGYVEASOLENIAQTL-----KDLGRKRAILIHG 217

QY 296 CNNMVEQELPGGGILIYQ 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 218 ANGMDEATLSGENI-IYE 234

RESULT 8
US-09-134-001C-5198
; Sequence 5198, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
```

```
Matches 45; Conservative 32; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLEMCMTGLDTKASVFFKTNADGNNTCA-----KEMT 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 59 FIQTNPQPFYFNKAMCVCGTGGDSNSP-----NISTTVAFVVASAGVPVIKHGNSIT 113

QY 192 KLSGISEIIPEMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGF-----SYAS 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 114 SHSGSTDVLHEMNIKTNKMEVEQQLN-LKGLAF-----ISATDSYPMMKLQSIKSIAT 168

QY 241 YEVMGLDATALSYGDLVKRVLGCGFSEF-SVAVTIFGGRGQAGTWGKEIGAE----AYD 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 PTIFNLIGLPLNPFKLTYYQVMGYVEASOLENIAQTL-----KDLGRKRAILIHG 217

QY 296 CNNMVEQELPGGGILIYQ 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 218 ANGMDEATLSGENI-IYE 234

RESULT 7
US-09-710-279-2244
; Sequence 2244, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2244
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-2244

Query Match      4.9%; Score 94.5; DB 4; Length 331;
Best Local Similarity 22.7%; Pred. No. 0.085;
Matches 45; Conservative 32; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLEMCMTGLDTKASVFFKTNADGNNTCA-----KEMT 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 59 FIQTNPQPFYFNKAMCVCGTGGDSNSP-----NISTTVAFVVASAGVPVIKHGNSIT 113

QY 192 KLSGISEIIPEMEICDFDFEPCGYSMNAIHGSAFSTIHVTPEDGF-----SYAS 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 114 SHSGSTDVLHEMNIKTNKMEVEQQLN-LKGLAF-----ISATDSYPMMKLQSIKSIAT 168

QY 241 YEVMGLDATALSYGDLVKRVLGCGFSEF-SVAVTIFGGRGQAGTWGKEIGAE----AYD 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 PTIFNLIGLPLNPFKLTYYQVMGYVEASOLENIAQTL-----KDLGRKRAILIHG 217

QY 296 CNNMVEQELPGGGILIYQ 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 218 ANGMDEATLSGENI-IYE 234

RESULT 8
US-09-134-001C-5198
; Sequence 5198, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
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; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5198
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5198

Query Match
Best Local Similarity 4.9%; Score 94.5; DB 3; Length 342;
Matches 45; Conservative 33; Mismatches 68; Indels 53; Gaps 9;

QY 147 YYATEYPEQPMVNLKMCMTGLDITKASVFFKTNADGNNTTCA-----KEMT 191
Db 70 FICTNPNOPFYNKAMCVCGTGGQNSF-----NISTTVAFVVASAGVPIKHGKNSIT 124

QY 192 KLSGISEIPEMEICDPDFEPCGYSMNAIHGSAFSTHVTPEDFG-----SYAS 240
Db 125 SHSGSTDVLHEMNIKTKMNEVEQQLN-LKGLAF-----ISATSYPMMKKLOIRKSIAT 179

QY 241 YEVMGLDATALSYGDLVKRYLVCFGPSEF-SVAVTIPGGRGQAGTWGKELGAE---AYD 295
Db 180 PTIFNLIGPLINFKLTQYQVMGVYEAQLENIAQTL-----KDLGRKRAILIHG 228

QY 296 CNMNVQELPGGGLIYQ 313
Db 229 ANGMDAATLSGENI-IYE 245

RESULT 9
US-09-248-796A-19513
; Sequence 19513, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19513
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19513

Query Match
Best Local Similarity 4.9%; Score 94.5; DB 4; Length 634;
Matches 65; Conservative 40; Mismatches 107; Indels 71; Gaps 15;

QY 40 SGRALSRQIDSVLDLARKIVIKTCGTTKLLTIPRILELAELSPLAAVKYSRGTFTI 99
Db 304 ANIRYLVLEADRMLDWGE-----PQIRYIVECDMP--AVK-DRQTLM 345

QY 100 FPGAQAPHRSEFEEVAVLNRYFGLKSGGNVYIGDAARPGQKWHYYATEYPEQPMVN 159
Db 346 FSG-----TFPRDIQMLARDF--LKD-----YVFLSVGRVGS-----TSENITQKILY 386

QY 160 LEMCMTGLDITKASV---PFKTNADGNNTTCAKEMTKLSGISEIPEMEICDPDFEPCGYS 216
Db 387 VE-----DDEKKSVIDLLSANENGLTIVFTETKNAD-----NLADYLDQ-GFP 431

QY 217 MNAIHGSAFSTHVTPEDFGFSYAEVWMLDATALSYGDL--VKRYLVCFGPSEFSVAVT 274

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Matches	95; Conservative	51; Mismatches	124; Indels	174; Gaps	24;
Qy	35	VDPHGG-----LRALSR-----QIDSVLDLA--RKIVIKTCGTTKLL---	72		
Db	861	VETHGTGRLGDPIEARALSDAYGGDREHPLRIGSVKSNIGHTQAAAGVAGLKLVLAMQ	920		
Qy	73	--TIPRIELAEELSPLAAVKYSRGTFIE--PGAQAPHRFSFSEBVLNVFEGGLKS	127		
Db	921	AGVLPRTLHADE-----PSPIDWSSGNAISLLQEPAAWAGERPRRACVS-----SFG--IS	970		
Qy	128	GGWAYVI-----GDAARPGQ-----KWHIYYAT-----EYEPQPMVN	159		
Db	971	GTNAHAIIIEBAPPTGDDTRPDRMPVVPVWLSASTGEALRAARLAGHLREHPDQ--D	1027		
Qy	160	LEMCMTGLDTPKKASVFKEKN--ADGNWTTCAKEMTKLSGISEIIPMEICDFDFEPCGYS	216		
Db	1028	LDDVAVSLATGTRAAALAYRSGFVPADASTAL-----RIIDEL-----AAGGS	1068		
Qy	217	MNAIHGSFAS--TIHVTPEDFGSYASYEVMGLD-----ATAL-----	251		
Db	1069	GDAVTGTARAPQRVWFVFCGGQWAGMADLLDGDPPFASVLRECADALEPYLDPEIVP	1128		
Qy	252	-----SYGDILKRVILGCGPSEFSVANVI-----FG-----GRGQ	281		
Db	1129	FLRAEAQRTPDHTLSTDRYDVVVQPVL-----FAVMVSLAARWRAYVEPAAVTHGSHQ	1181		
Qy	282	-----ACTWGKELGAEAYDCNNMVEQLPGGGILIIYGFCAAEADAVA-----	323		
Db	1182	GETAAACVAGALSILDDAARAVALRSRVIAIATPANGAM--ASIAASVDVEAARDGRVEIA	1239		
Qy	324	--SSPKSVLRCPFGENAAAPFAKDC	345		
Db	1240	AVNGPRAVVVGSGDRDLDRLVASC	1263		

RESULT 12
US-08-008-688A-2
; Sequence 2, Application US/08008688A
; Patent No. 5462862
; GENERAL INFORMATION:
; APPLICANT: Martinus A. M. Groenen
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Pieter Van Solingen
; APPLICANT: Bertus P. Koekman
; APPLICANT: Lucia H. M. Van Der Voort
; APPLICANT: Juan F. Martin
; APPLICANT: Santiago Gutierrez
; APPLICANT: Bruno Diez
; APPLICANT: Emilio Alvarez
; APPLICANT: Jose L. Barredo
; APPLICANT: Christina Esmahan
; TITLE OF INVENTION: A METHOD FOR ENHANCING PRODUCTION OF
; TITLE OF INVENTION: SECONDARY METABOLITES USING
; TITLE OF INVENTION: CLUSTERED BIOSYNTHETIC GENES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; FILING APPLICATION NUMBER: US/08/008,688A
; FILING DATE: 19930125
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 07/392,119

```

; FILING DATE: August 10, 1989
; APPLICATION NUMBER: EPO 88201714.8
; FILING DATE: August 11, 1988
; APPLICATION NUMBER: EPO 89201044.8
; FILING DATE: April 21, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: 05939/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-5277
; TELEFAX: (415) 854-0875
; TELEX: ---
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; US-08-008-688A-2

Query Match 4.5%; Score 86.5; DB 1; Length 355;
Best Local Similarity 22.7%; Pred. No. 0.78;
Matches 82; Conservative 45; Mismatches 117; Indels 117; Gaps 21;

Qy 17 FE-GYKRRLUITSEAPVFVDPHGSLRLRSQIDSVLDLARKIVIKTCGTTKLLLT-I 74
Db 9 FEIGYE-----HGSAAKAVIARSIDFAVDLIRGKTKKDEELKQVLSQL 52
Qy 75 PRILE-----LABELSMPLAAVKYSGRTFFPCAQAPHRFSFEEVAVLN---RYFGGLK 126
Db 53 GRVIERWPKYEEI-----RG--IAKGAE---RDVG-EIVMLNTRTEFAYGLK 95
Qy 127 SGGN----AVV-IGDAARPGQKHYYATYEYPEOPMVNLEMCMTGIDTKKASVFFKTNAD 181
Db 96 AARDGGTTAYCQUPNGALOGQNTDFPSAT---KENLIRLTIRAGLPTIK----FITEA- 147
Qy 182 GNTTCAKEMTKLSGISEIIPEMEICDFDEPFCGYSMNAIHGSAFSTIHVTPEDGFSYASY 241
Db 148 -----GI-----IGKVFNSAGVAVN-----YNAL 167
Qy 242 EVNGLDATALSYGDLVKRVLCGPGSEFSVAVTIFGGRG-----QAGTWGKELGAEAYDC 296
Db 168 HLQGLRPTGPVSHIALRIALESTSPSQAYDRIVEQGGMAASAFIMVGNHGEAFGLE-FSP 226
Qy 297 NNWVEQLPGGTLIYOSFCAA-----EDAVASSPKS-----VLRCFDCGENAAPFA 342
Db 227 TSIRKQVLDANGRMVHTNHCLLQHGKNEKELDPLPDSWNHRQRMFLLDGDGTGKQK-FA 285
Qy 343 K 343
Db 286 Q 286

RESULT 13
US-09-604-957-4
; Sequence 4, Application US/09604957
; Patent No. 6486314
; GENERAL INFORMATION:
; APPLICANT: VAN GEEL-SCHUTTEN, GERITDINA HENDRIKA
; APPLICANT: DIJKHUIZEN, LUBBERT
; APPLICANT: RAHAOUI, HAKIM
; APPLICANT: LEER, ROBERT-JAN
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASE AND NOVEL GLUCAN
; FILE REFERENCE: BO 4388
; CURRENT APPLICATION NUMBER: US/09/604,957.
; CURRENT FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 00201871.1
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4

```

```
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-604-957-4

Query Match      4.5%; Score 86.5; DB 4; Length 545;
Best Local Similarity 22.5%; Pred. No. 1.6;
Matches 73; Conservative 50; Mismatches 137; Indels 65; Gaps 17;

QY 33 VFVDPHSGRLALSRQIDSVLDLARKIVIKTCGTTKLLTIPRIILELAELSMPAAVK 92
Db 158 IFIRAHDSVQTVIAKIKA-----QINPKTDGLTFTLDELQAQFIYNE-DMRQAKK 210

QY 93 YSRGTTFPGAQAPHR-SFSEVAVLNRYFGGLKSGGNAYVIG-----DAARPGQKWHI 146
Db 211 YTQSN-----PTAVALMSLNKDSITRLYGYDMYSDGQYMATKSPYYDAITLLKARI 264

QY 147 YYAT-----EYPEQPMVNLKMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEI 199
Db 265 KYAAGQDMKITTVGDKSHMDYTGVLV---SVRYGTGANATDQGSATKTQGNVAVI 321

QY 200 I---PEMEICDFPEPCGYSMNAIH-GSAFSTIHVTPEDGF-SYASVEVNMGLDATALSY- 253
Db 322 TSNNPSLKLQND--KVIVNMGAAHKNQEVRLPILLTTKDLGTSYTS-----DAAAKSLY 373

QY 254 -----GDLV---KRVLGCFGP---SEFSVAVTIFFGRGQ-----AGTWGKELGAEAYDCN 297
Db 374 RKTNDKGLVFDASDIQGYLNPQVSGYLAVWVPVGASDNDQVRVAASNKANATGQVYESS 433

QY 298 NMVEQELPGGGILLYOSFCAAEADAV 322
Db 434 SALDSQ-----LIYEGFSNFQDFV 452

RESULT 14
US-09-008-172-2
; Sequence 2, Application US/09008172
; Patent No. 6127602
; GENERAL INFORMATION:
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Substitutes for Modified Starch and
; FILE REFERENCE: 0358D
; CURRENT APPLICATION NUMBER: US/09/008,172
; EARLIER FILING DATE: 1998-01-16
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1430
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-008-172-2

Query Match      4.5%; Score 86.5; DB 3; Length 1430;
Best Local Similarity 22.5%; Pred. No. 8.2;
Matches 73; Conservative 50; Mismatches 137; Indels 65; Gaps 17;

QY 33 VFVDPHSGRLALSRQIDSVLDLARKIVIKTCGTTKLLTIPRIILELAELSMPAAVK 92
Db 578 IFIRAHDSVQTVIAKIKA-----QINPKTDGLTFTLDELQAQFIYNE-DMRQAKK 630

QY 93 YSRGTTFPGAQAPHR-SFSEVAVLNRYFGGLKSGGNAYVIG-----DAARPGQKWHI 146
Db 631 YTQSN-----PTAVALMSLNKDSITRLYGYDMYSDGQYMATKSPYYDAITLLKARI 684

QY 147 YYAT-----EYPEQPMVNLKMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEI 199
Db 685 KYAAGQDMKITTVGDKSHMDYTGVLV---SVRYGTGANATDQGSATKTQGNVAVI 741

QY 200 I---PEMEICDFPEPCGYSMNAIH-GSAFSTIHVTPEDGF-SYASVEVNMGLDATALSY- 253
Db 742 TSNNPSLKLQND--KVIVNMGAAHKNQEVRLPILLTTKDLGTSYTS-----DAAAKSLY 793

QY 254 -----GDLV---KRVLGCFGP---SEFSVAVTIFFGRGQ-----AGTWGKELGAEAYDCN 297
Db 794 RKTNDKGLVFDASDIQGYLNPQVSGYLAVWVPVGASDNDQVRVAASNKANATGQVYESS 853

QY 298 NMVEQELPGGGILLYOSFCAAEADAV 322
Db 854 SALDSQ-----LIYEGFSNFQDFV 872

Query Match      4.5%; Score 86.5; DB 3; Length 1430;
Best Local Similarity 22.5%; Pred. No. 8.2;
Matches 73; Conservative 50; Mismatches 137; Indels 65; Gaps 17;

QY 33 VFVDPHSGRLALSRQIDSVLDLARKIVIKTCGTTKLLTIPRIILELAELSMPAAVK 92
Db 578 IFIRAHDSVQTVIAKIKA-----QINPKTDGLTFTLDELQAQFIYNE-DMRQAKK 630

QY 93 YSRGTTFPGAQAPHR-SFSEVAVLNRYFGGLKSGGNAYVIG-----DAARPGQKWHI 146
Db 631 YTQSN-----PTAVALMSLNKDSITRLYGYDMYSDGQYMATKSPYYDAITLLKARI 684

QY 147 YYAT-----EYPEQPMVNLKMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEI 199
Db 685 KYAAGQDMKITTVGDKSHMDYTGVLV---SVRYGTGANATDQGSATKTQGNVAVI 741

QY 200 I---PEMEICDFPEPCGYSMNAIH-GSAFSTIHVTPEDGF-SYASVEVNMGLDATALSY- 253
Db 742 TSNNPSLKLQND--KVIVNMGAAHKNQEVRLPILLTTKDLGTSYTS-----DAAAKSLY 793

QY 254 -----GDLV---KRVLGCFGP---SEFSVAVTIFFGRGQ-----AGTWGKELGAEAYDCN 297
Db 794 RKTNDKGLVFDASDIQGYLNPQVSGYLAVWVPVGASDNDQVRVAASNKANATGQVYESS 853

QY 298 NMVEQELPGGGILLYOSFCAAEADAV 322
Db 854 SALDSQ-----LIYEGFSNFQDFV 872

Search completed: May 11, 2005, 22:53:52
Job time : 25.3436 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:36:02 ; Search time 93.8969 Seconds
(without alignments)
1515.788 Million cell updates/sec

Title: US-10-732-923-407

Perfect score: 1914

Sequence: 1 MAVLSAAGAPPASAIQFEY.....NLVCLFEXDAIEEKDGLVDS 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1990s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1853	96.8	366	8	Adm48039 Polypepti
2	1726	90.2	400	8	Adm48040 Polypepti
3	862.5	45.1	237	7	Abm73860 DNA clone
4	804.5	42.0	360	2	Aar75006 Tomato S-
5	802	41.9	363	5	Aau79674 Cucurbita
6	802	41.9	363	5	Abg75228 Plant wit
7	802	41.9	363	8	Adp90956 Fig leaf g
8	802	41.9	363	8	Adr38366 Fig leaf
9	771.5	40.3	366	3	Agg28816 Arabidops
10	737	38.5	309	7	Abm73938 DNA clone
11	455	23.8	155	7	Abm74096 DNA clone
12	425.5	22.2	215	3	Agg28817 Arabidops
13	393.5	20.6	184	3	Agg28818 Arabidops
14	377.5	19.7	368	8	Adn22644 Bacterial
15	377.5	19.7	368	8	Adn22643 Bacterial
16	360.5	18.8	348	3	Aab56589 Human pro
17	359	18.8	348	4	Abg05997 Novel hum
18	356.5	18.6	334	5	Aau84313 Protein A
19	356.5	18.6	334	7	Adg60574 Human Pro
20	356.5	18.6	334	7	Adg48325 Human Pro
21	356.5	18.6	334	7	Adg60570 Human Pro
22	356.5	18.6	334	7	Adn48321 Human Pro
23	356.5	18.6	334	8	Adn03708 Antipori
24	356.5	18.6	334	8	Adq88208 Human 912
25	356.5	18.6	347	4	Abb61186 Drosophil

ALIGNMENTS

RESULT 1
ADM48039
ID ADM48039 standard; protein; 366 AA.

AC ADM48039;

DT 03-JUN-2004 (first entry)

DE Polypeptide sequence #89 useful in producing transgenic plants.

XX Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;

KW osmotic stress; sugar transport; cell cycle pathway; plant height;

KW carbohydrate transport; crop productivity; plant growth;

KW stress resistance; disease resistance; insect resistance; heat tolerance;

KW nitrogen assimilation; water stress tolerance;

KW photosynthetic carbon fixation; virus resistance; gene therapy.

XX Zea mays.

OS US2003233670-A1.

PN 18-DEC-2003.

PD 04-DEC-2002; 2002US-00310154.

PP 04-DEC-2001; 2001US-0337358P.

PR (EDGE/) EDGERTON M D.

PA (CHOM/) CHOMET P S.

PA (LACC/) LACCETTI L B.

PI Edgerton MD, Chomet PS, Laccetti LB;

XX WPI; 2004-061374/06.

DR N-PSDB; ADM47671.

XX New polynucleotide, useful for manipulating plant protein quality,
PT improving plant growth, yield and crop productivity or grain composition
PT or producing plants with improved properties.

XX Claim 8; SEQ ID NO 457; 144pp; English.

XX The present invention relates to polynucleotide sequences, and the
CC proteins they encode. The sequences are isolated from a variety of
CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
CC soybean, and wheat), cyanobacteria, bacteria, yeast and other fungi. The
CC polynucleotide and polypeptide sequences of the invention are useful in
CC the production of transgenic plants that have improved properties. Also

CC disclosed are methods of producing fertile transgenic plants, preferably
 CC maize, with desired phenotypes. The polynucleotide and polypeptide
 CC sequences are useful for improving plants by providing protection against
 CC osmotic stress, improving altering sugar transport and/or metabolism,
 CC modifying the cell cycle pathway, reducing plant height, modifying
 CC carbohydrate transport, improving crop productivity, improving plant
 CC growth and stress resistance, improving disease resistance, improving
 CC insect resistance, improving cold or heat tolerance, improving nitrogen
 CC assimilation, improving stalk strength, improving water stress tolerance,
 CC improving photosynthetic carbon fixation, improving biotic and abiotic
 CC stress resistance, improving resistance to oxidative stress, providing
 CC increased vigour, reducing senescence, and conferring virus resistance.
 CC The present sequence represents a polypeptide sequence of the invention.
 CC Note: The sequence data for this patent is not provided in the printed
 CC specification but is obtained in electronic format from the USPTO website
 CC at seqdata.uspto.gov.

XX
 SQ Sequence 366 AA;
 Query Match 96.8%; Score 1853; DB 8; Length 366;
 Best Local Similarity 100.0%; Pred. No. 2.2e-192;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVLSAAGAPPASAIIGFEGYEKLEITFSEAPVFDPHGSLRALSRQSDSVLDLARKI 60
 DB 1 MAVLSAAGAPPASAIIGFEGYEKLEITFSEAPVFDPHGSLRALSRQSDSVLDLARKI 60
 QY 61 VIKTCGTTKLLLTIPRILELAELSMPAAVKYSRGTFIPPGAQAPHRFSFSEAVLNR 120
 DB 61 VIKTCGTTKLLLTIPRILELAELSMPAAVKYSRGTFIPPGAQAPHRFSFSEAVLNR 120
 QY 121 YFGLKSGGNAYVIGDAARPGQWHIYYATEYEPQWNLNEMCMTGLDTKKASVFFKTN 180
 DB 121 YFGLKSGGNAYVIGDAARPGQWHIYYATEYEPQWNLNEMCMTGLDTKKASVFFKTN 180
 QY 181 DGNNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSNNAIHGSAFSTIHTVPDGFYSAS 240
 DB 181 DGNNTTCAKEMTKLSGISEIIPMEICDFPEPCGYSNNAIHGSAFSTIHTVPDGFYSAS 240
 QY 241 YEVMGLDATALSYGDLVKRVLCGFGSFSFSAVTIFGGRGQAGTWGKELGAEAYDCNNMV 300
 DB 241 YEVMGLDATALSYGDLVKRVLCGFGSFSFSAVTIFGGRGQAGTWGKELGAEAYDCNNMV 300
 QY 301 EQELPGGGLIYQSFCAAEADAVASSPKSVLRCTFDGENAAPPFAKCKLANLVCL 355
 DB 301 EQELPGGGLIYQSFCAAEADAVASSPKSVLRCTFDGENAAPPFAKCKLANLVCL 355

RESULT 2
 ADM48040
 ID ADM48040 standard; protein; 400 AA.
 XX
 AC ADM48040;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Polypeptide sequence #90 useful in producing transgenic plants.
 XX
 KW plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic;
 KW osmotic stress; sugar transport; cell cycle pathway; plant height;
 KW carbohydrate transport; crop productivity; plant growth;
 KW stress resistance; disease resistance; insect resistance; heat tolerance;
 KW nitrogen assimilation; water stress tolerance;
 KW photosynthetic carbon fixation; virus resistance; gene therapy.
 XX
 OS Zea mays.
 XX
 XX US2003233670-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 04-DEC-2002; 2002US-00310154.
 XX
 XX

PR 04-DEC-2001; 2001US-0337358P.
 XX
 PA (EDGE/) EDGERTON M D.
 PA (CHOM/) CHOMET P S.
 PA (LACC/) LACCETTI L B.
 XX
 PI Edgerton MD, Chomet PS, Laccetti LB;
 XX
 DR WPI; 2004-061374/06.
 DR N-PSDB; ADM47672.
 XX
 PT New polynucleotide, useful for manipulating plant protein quality,
 PT improving plant growth, yield and crop productivity or grain composition
 PT or producing plants with improved properties.
 XX
 PS Claim 8; SEQ ID NO 458; 144pp; English.
 XX
 CC The present invention relates to polynucleotide sequences, and the
 CC proteins they encode. The sequences are isolated from a variety of
 CC organisms such as plants (e.g. maize, rice, sorghum, thale cress,
 CC soybean, and wheat), cyanobacteria, bacteria, and other fungi. The
 CC polynucleotide and polypeptide sequences of the invention are useful in
 CC the production of transgenic plants that have improved properties. Also
 CC disclosed are methods of producing fertile transgenic plants, preferably
 CC maize, with desired phenotypes. The polynucleotide and polypeptide
 CC sequences are useful for improving plants by providing protection against
 CC osmotic stress, improving altering sugar transport and/or metabolism,
 CC modifying the cell cycle pathway, reducing plant height, modifying
 CC carbohydrate transport, improving crop productivity, improving plant
 CC growth and stress resistance, improving disease resistance, improving
 CC insect resistance, improving cold or heat tolerance, improving nitrogen
 CC assimilation, improving stalk strength, improving water stress tolerance,
 CC improving photosynthetic carbon fixation, improving biotic and abiotic
 CC stress resistance, improving resistance to oxidative stress, providing
 CC increased vigour, reducing senescence, and conferring virus resistance.
 CC The present sequence represents a polypeptide sequence of the invention.
 CC Note: The sequence data for this patent is not provided in the printed
 CC specification but is obtained in electronic format from the USPTO website
 CC at seqdata.uspto.gov.

XX
 SQ Sequence 400 AA;
 Query Match 90.2%; Score 1726; DB 8; Length 400;
 Best Local Similarity 84.5%; Pred. No. 1.7e-178;
 Matches 338; Conservative 8; Mismatches 22; Indels 32; Gaps 3;
 QY 1 MAVLSAAGAPPASAIIGFEGYEKLEITFSEAPVFDPHGSLRALSRQSDSVLDLARKI 58
 DB 1 MAVLSAAGAPPASAIIGFEGYEKLEITFSEAPVFDPHGSLRALSRQSDSVLDLARKI 60
 QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSMPAAVKY 93
 DB 61 IVSELSNKKDFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSMPAAVKY 120
 QY 94 SRTGTFIPGAQAPHRFSFSEAVLNRVYFGLKSGGNAYVIGDAARPGQWHIYYATEY 153
 DB 121 SRTGTFIPGAQAPHRFSFSEAVLNRVYFGLKSGGNAYVIGDAARPGQWHIYYATEY 180
 QY 154 EQPMVNLNEMCMTGLDTKKASVFFKTNADGNNTTCAKEMTKLSGISEIIPMEICDFDPEPC 213
 DB 181 EQPMVNLNEMCMTGLDTKKASVFFKTNADGNNTTCAKEMTKLSGISEIIPMEICDFDPEPC 240
 QY 214 GYSMNAIHGSAFSTIHTVPDGFYSASYEVMGLDATALSYGDLVKRVLCRFGSFSFSAV 273
 DB 241 GYSMNAIHGSAFSTIHTVPDGFYSASYEVMGLDATALSYGDLVKRVLCRFGSFSFSAV 300
 QY 274 TIFGGRGQAGTWGKELGAEAYDCNNMVVEQLPGGGLIYQSFCAAEADAVASSPKSVLR 333
 DB 301 TIFGGRGQAGTWGKELGAEAYDCNNMVVEQLPGGGLIYQSFCAAEADAVASSPKSVLR 360
 QY 334 DGENA-----APFAKCKLANLVCL-EEXDAIEEKDGVLE 368
 DB 361 DGENVESAPPMKKDYKLANLLCWEEEADEAMEEKAGVLDE 400


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Best Local Similarity 46.0%; Pred. No. 6.4e-78;
Matches 180; Conservative 52; Mismatches 85; Indels 74; Gaps 10;

QY 11 PASAIGFEGYKRLKLEITFSEAPVFDVPHGSGRLSRQSDSVLDLAR-----58
Db 4 PTAIGFEGYKRLKLEVSFFPGIFADPRGMGLRSLKAQDLDTLAECTIVDSLSNDYL 63
QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSMLAAVKYSRGTFFPGA 103
Db 64 DSVLSESSLFVVPYKFIKTCGTTKLLLSIPALIKLADSLSNVKSRYTRGSFIFPGA 123
QY 104 QPAPHRSPSEEVAVLNRYFGLKSGGNAYVIG--DAARPGQKWHIYAT-----EYEPQPM 157
Db 124 QSPFHRSPSEEVAVLDGYLAKLHGSAYVMGSPDETR---KWHVYSACAKMGRSRYNPV 180
QY 158 VNLKEMCMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPCGYSM 217
Db 181 YTLKEMCMTGLDKKASVFFKTT---DTSSAAAMTENSIGIRKLPKSDICDFDFPCGYSM 236
QY 218 NAIHGSFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSVAVTIFG 277
Db 237 NAIHGSFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSVAVTIFG 277
QY 278 GRQAGTWGKE-----LGAEAYDCNMVQEQLPGGGILYQSFCAEDAVASSPKSVL- 330
Db 293 ---HSDVVGEDLKDLDLKGEGEKSCMLGENGSVIYQSFKNRGD-YASSPRSLM 348
QY 331 RCFDGENAAPPFAKCKLANLVCLLEEXDAIEE 361.
Db 349 KC-----CWREDEADEE 360

RESULT 7
ADP90956
ID ADP90956 standard; protein; 363 AA.
AC ADP90956;
XX
XX
XX 23-SEP-2004 (first entry)
XX
XX Figleaf gourd S-adenosylmethionine decarboxylase (SAMDC) 1814 protein.
XX plant; environmental stress resistance; polyamine promoter; fat; oil;
XX cellulose; hydrocarbon; pigment; enzyme production; natural rubber;
XX pharmaceutical; figleaf gourd; S-adenosylmethionine decarboxylase;
XX SAMDC 1814; enzyme; EC 4.1.1.50.
XX Cucurbita ficifolia.
XX OS
XX JP2004180588-A.
XX PN
XX 02-JUL-2004.
XX PD
XX 03-DEC-2002; 2002JP-00351750.
XX PF
XX 03-DEC-2002; 2002JP-00351750.
XX PR
XX (TOYO-) TOYOBO SOGO KENKYUSHO KK.
XX PA
XX WPI; 2004-472277/45.
XX DR
XX N-PSDB; ADP90955.
XX DD
XX Novel plant exhibiting improved environmental stress resistance and
XX having nucleic acid controlling amount of polyamines, useful for
XX obtaining substances such as fat and oil, cellulose, and natural rubber.
XX PT
XX Example 1; SEQ ID NO 4; 69pp; Japanese.
XX PS
XX The invention relates to a novel plant, or its offspring, exhibiting
XX improved environmental stress resistance and having a nucleic acid which
XX controls the amount of polyamines under the control of a promoter that
XX functions in the plant, compared with the plant which does not possess
XX the nucleotide and where the nucleotide is maintained stably within the
XX CC
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CC plant. The polynucleotide of the invention may be useful for obtaining
CC substances such as fat and oil, cellulose, hydrocarbon, pigment, enzymes,
CC natural rubber and pharmaceutical compounds. The plant has improved
CC oxidative stress, herbicide, salt, osmotic pressure, water or low
CC temperature resistance. The current sequence is that of the figleaf gourd
CC S-adenosylmethionine decarboxylase (SAMDC) 1814 protein of the invention.
XX
XX Sequence 363 AA;
Query Match 41.9%; Score 802; DB 8; Length 363;
Best Local Similarity 46.0%; Pred. No. 6.4e-78;
Matches 180; Conservative 52; Mismatches 85; Indels 74; Gaps 10;

QY 11 PASAIGFEGYKRLKLEITFSEAPVFDVPHGSGRLSRQSDSVLDLAR-----58
Db 4 PTAIGFEGYKRLKLEVSFFPGIFADPRGMGLRSLKAQDLDTLAECTIVDSLSNDYL 63
QY 59 -----KIVIKTCGTTKLLLTIPRILELAELSMLAAVKYSRGTFFPGA 103
Db 64 DSVLSESSLFVVPYKFIKTCGTTKLLLSIPALIKLADSLSNVKSRYTRGSFIFPGA 123
QY 104 QPAPHRSPSEEVAVLNRYFGLKSGGNAYVIG--DAARPGQKWHIYAT-----EYEPQPM 157
Db 124 QSPFHRSPSEEVAVLDGYLAKLHGSAYVMGSPDETR---KWHVYSACAKMGRSRYNPV 180
QY 158 VNLKEMCMTGLDTKKASVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPCGYSM 217
Db 181 YTLKEMCMTGLDKKASVFFKTT---DTSSAAAMTENSIGIRKLPKSDICDFDFPCGYSM 236
QY 218 NAIHGSFSTIHTVPEDGFSYASYEVNGLDATALSYGDLVKRVLCGFGPSEFSVAVTIFG 277
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QY 278 GRQAGTWGKE-----LGAEAYDCNMVQEQLPGGGILYQSFCAEDAVASSPKSVL- 330
Db 293 ---HSDVVGEDLKDLDLKGEGEKSCMLGENGSVIYQSFKNRGD-YASSPRSLM 348
QY 331 RCFDGENAAPPFAKCKLANLVCLLEEXDAIEE 361
Db 349 KC-----CWREDEADEE 360

RESULT 8
ADP90956
ID ADP90956 standard; protein; 363 AA.
AC ADP90956;
XX
XX 18-NOV-2004 (first entry)
XX
XX Fig leaf gourd S-adenosylmethionine decarboxylase (SAMDC) protein SeqID 4.
XX transgenic; plant; productivity; polyamine metabolism; fig leaf gourd;
XX S-adenosylmethionine decarboxylase; SAMDC; enzyme.
XX Cucurbita ficifolia.
XX OS
XX JP2004242510-A.
XX PN
XX 02-SEP-2004.
XX PD
XX 10-FEB-2003; 2003JP-00032606.
XX PF
XX 10-FEB-2003; 2003JP-00032606.
XX PR
XX (TOYO-) TOYOBO SOGO KENKYUSHO KK.
XX PA
XX WPI; 2004-608540/59.
XX DR
XX N-PSDB; ADP90955.
XX DD
XX Enhanced plant e.g. sweet potato, has transgenic plant with better
XX productivity and character regardless of cultivation environment compared
XX to plant without nucleic acid.
XX PT
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AAG28817
ID AAG28817 standard; protein; 215 AA.
XX
AC AAG28817;
XX
DT DT
DE 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34177.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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PR 08-APR-1999; 99US-0128714P.
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;	KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.	KW	termination sequence.
XX		XX	
OS	Arabidopsis thaliana.	OS	Arabidopsis thaliana.
XX		XX	
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PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 20.6%; Score 393.5; DB 3; Length 184;

Best Local Similarity 46.4%; Pred. No. 6.9e-34;

Matches 90; Conservative 24; Mismatches 57; Indels 23; Gaps 6;

Qy 162 MCMTGTLDTKCAVFFKTNADGNTTCAKEMTKLSGISIIPEMICDPDFPFCGYSMNAIH 221

Db 1 MCMTGDLREKAAVFKDEADKTGS---MTDNGIRKILPKSIBICDFEPEPCGYSMNSIE 56

Qy 222 GSASFSTIHVTPEDGFSYASVYEVNGLDATALSYGDLVKRVLCGFCGPSEFSVAVTIFGRGQ 281

Db 57 GDAISTIHVTPEDGFSYASVYEVNGLDATALSYGDLVKRVLCGFCGPSEFSVAVTIFGRGQ 113

XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 5296; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 368 AA;

Query Match 19.7%; Score 377.5; DB 8; Length 368;
Best Local Similarity 32.3%; Pred. No. 1.1e-31;
Matches 108; Conservative 57; Mismatches 92; Indels 77; Gaps 16;
QY 17 FEGYKRLKLTTFSEAPVFVDPHGSLRALRSOIDSVLDLAR----- 58
Db 25 FEGAELLELWFCSS---TQNETRSLRIIPREIDAMLDIARCKILHSHKINESIDSYVLS 81
QY 59 -----KIVIKTCGTTKLLTIPRIELEABELS--MPLAAVKYSRGTFFPFGQAPAP 107
Db 82 ESSLFTSDNRVILKTCGTTFLAALPVMQAGAYAGLDQVQSVYSRKNFLRPDLQPSL 141
QY 108 HRSFSEVAVLNRYFGLKSGGNAYVIGDAARPGQKWHY---YATEYP--EOPMVNLEM 162
Db 142 HKNFDAEVEYLDGFF----VDGHAYCLGSLKQ--DRWLYTFHREVEFFPAHKQPDHTLEI 195
QY 163 CMTGLDTKASVFETNA-DGNTTCAKEMTKLSGISIETPE-MEICDFDFPCGYSNNAI 220
Db 196 LMSDLDEEVLUHKTQYAVDGNDFWR-----AGIDKIIPAGADVHDELDFPCGYSNNAY 250
QY 221 HGSA--FSTIHTVPEDGFSYASVEVMGLDATALSYGDLV-----KRVLCFGSPSEFSVA 272
Db 251 MNDTDQYATHVTPKAFSPASE-----TNQDLVCLYSQTRKVLQCFRPNK--IL 299
QY 273 VTIFGGRGQAGTWGKELGABAYDCNNMVEQLPG 306
Db 300 MTVFA--NDISEKGDAQQQLWD-----RELPG 325

Search completed: May 11, 2005, 22:47:50
Job time : 95.8969 secs

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OM protein - protein search, using sw model

Run on: May 11, 2005, 22:38:57 ; Search time 94.5017 Seconds
(without alignments)
2167.492 Million cell updates/sec

Title: US-10-732-923-408

Perfect score: 2097

Sequence: 1 MAVLSAADASPVSAIGFEGY.....LLCWEEDADMBEKAGVLDE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2097	100.0	400	1	DCAM MAIZE
2	1715	81.8	398	1	DCAM ORYZA
3	1715	81.8	398	2	O7XT83
4	1682.5	80.2	393	1	DCAM HORCH
5	1663	79.3	392	2	O92FJ1
6	1632	77.8	395	2	O6K9B8
7	1632	77.8	395	2	O9SC67
8	1357	64.7	392	2	O6FAN6
9	1338.5	63.8	370	2	O84LA2
10	1300	62.0	369	2	O944U3
11	1290	61.5	319	2	O9F8M2
12	1000	47.7	358	2	O7XZQ9
13	980	46.7	357	1	DCAM CATRO
14	969	46.2	361	1	DCAM NICSY
15	969	46.2	361	1	DCAM TOBAC
16	969	46.2	362	1	DCAM DATST
17	968.5	46.2	374	2	O8S2S8
18	966	46.1	358	2	O8S2S9
19	965.5	46.0	353	1	DCAM VICFA
20	962	45.9	362	1	DCAM IPONI
21	961.5	45.9	363	1	DCAM SPOL
22	960.5	45.8	361	2	O8LKJ7
23	960	45.8	362	1	DCAM IPOBA
24	954	45.5	377	1	DCA2 DIACA
25	952	45.4	349	2	O9LSU6
26	950	45.3	354	2	O8W3Y2
27	946.5	45.1	353	1	DCAM PEA
28	944	45.0	381	1	DCAL DIACA
29	941.5	44.9	360	1	DCAM SOLTU
30	919.5	43.8	355	2	O8S3F8
31	915.5	43.7	361	2	O6RUQ3

32	909.5	43.4	361	1	DCAM DAUCA	O9axe3 daucus caro
33	881	42.0	366	1	DCAL ARATH	O96286 arabidopsis
34	879	41.9	361	1	DCAM HELAN	O65354 helianthus
35	876.5	41.8	369	2	O6S2S4	O6a284 brassica ju
36	876	41.8	366	2	O940Q5	O94005 arabidopsis
37	874.5	41.7	369	1	DCAL BRAJU	O49972 brassica ju
38	869.5	41.5	362	1	DCAL ARATH	O98759 arabidopsis
39	869.5	41.5	367	1	DCAL BRAJU	O98d88 brassica ju
40	869	41.4	366	2	O6QJ69	O6qj69 brassica ju
41	829	39.5	368	1	DCAL BRAJU	O42613 brassica ju
42	794	37.9	309	2	O6KC47	O6kc47 prunus pers
43	769	36.7	169	2	O9SC65	O9sc65 oryza sativ
44	697	33.2	228	2	O8VX33	O8vx33 vitis vinif
45	695.5	33.2	279	2	O76KV7	O76kv7 pisum sativ

ALIGNMENTS

RESULT 1

ID	DCAM MAIZE	STANDARD	PRT	400 AA
AC	O24575			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)			
DE	(SambC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].			
GN	Name=SAMDC;			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.			
OX	NCBI_TaxID=4577;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Michael A.J.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).			
CC	-1- COFACTOR: Pyruvoyl group (By similarity).			
CC	-1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.			
CC	-1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.			
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CC	EMBL; Y07767; CAA69075.1; -			
DR	PIR; T03947; T03947.			
DR	HSSP; P17707; LJEN.			
DR	InterPro; IPR001985; SAM decarbox.			
DR	Pfam; PF01536; SAM decarbox; 1.			
DR	ProDom; PD002379; SAM decarbox; 1.			
DR	TIGRFAMs; TIGR00535; SAM DCase; 1.			
DR	PROSITE; PS01336; ADOMETDC; 1.			
KW	Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.			
FT	CHAIN 1 77			
FT	CHAIN 78 400			
FT	CHAIN 77 78			
FT	SITE 77 78			
FT	MOD_RES 78 78			
FT	ACT_SITE 18 18			
FT	ACT_SITE 21 21			
FT	ACT_SITE 92 92			

SQ SEQUENCE 400 AA; 43515 MW; 1B2445775R55714A CRC64;
Query Match 100.0%; Score 2097; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 9.6e-170;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAVLSAADASPVSAGIFEGYKLEITFSEAPVFDVDPHGRLRALSGRAQIDSVLDLART 60
DB 1 MAVLSAADASPVSAGIFEGYKLEITFSEAPVFDVDPHGRLRALSGRAQIDSVLDLART 60
QY 61 IVSELSNKFDSYLVSESSIFLYPLKIVIKTCCTTKLLLTIPRIELAEELSPLAAVKY 120
DB 61 IVSELSNKFDSYLVSESSIFLYPLKIVIKTCCTTKLLLTIPRIELAEELSPLAAVKY 120
QY 121 SRTGTFPGAQAPAPHSFSEVAALNRYFGGLKSGGNVYIGDPPARPGQKWHVYFATEYP 180
DB 121 SRTGTFPGAQAPAPHSFSEVAALNRYFGGLKSGGNVYIGDPPARPGQKWHVYFATEYP 180
QY 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
DB 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
QY 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSEFSVAV 300
DB 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSEFSVAV 300
QY 301 TIFGGRGHAGTWKALGAEVYDNNVVEQLPQGLLVYQSFCAAEADVATSPKSVFHC 360
DB 301 TIFGGRGHAGTWKALGAEVYDNNVVEQLPQGLLVYQSFCAAEADVATSPKSVFHC 360
QY 361 DGENVESAPPPMKDYKLANLLCWEEBDAAMEEKAGVLDE 400
DB 361 DGENVESAPPPMKDYKLANLLCWEEBDAAMEEKAGVLDE 400

RESULT 2

DCAM_ORYSA STANDARD; PRT; 398 AA.
ID O24215; O81269;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
GN Name=SAMDC;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica / Nipponbare;
RX MEDLINE=21066059; PubMed=11139406; DOI=10.1042/0264-6021.3530403;
RA Franceschetti M., Hanfrey C., Scaramagli S., Torrigiani P., Bagni N.,
RA Michael A.J.;
RT "Characterization of monocot and dicot plant S-adenosyl-L-methionine
RT decarboxylase gene families including identification in the mRNA of a
RT highly conserved pair of upstream overlapping open reading frames.";
RL Biochem. J. 353:403-409(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Li Z.Y., Chen S.Y.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -1- COFACTOR: Pyruvoyl group.
CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; Y07766; CAA69074.2; -.
DR EMBL; AF067194; AAC79990.1; -.
DR HSSP; P17707; I172.
DR Gramene; O24215; -.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 77 S-adenosylmethionine decarboxylase beta
FT CHAIN 78 398 chain (By similarity).
FT SITE 77 78 S-adenosylmethionine decarboxylase alpha
FT MOD_RES 78 78 chain (By similarity).
FT ACT_SITE 18 18 Pyruvic acid (Ser) (By similarity).
FT ACT_SITE 21 21 By similarity.
FT ACT_SITE 92 92 By similarity.
FT CONFLICT 250 250 S -> L (in Ref. 2).
SQ SEQUENCE 398 AA; 43283 MW; BC24F359962F8655 CRC64;
Query Match 81.8%; Score 1715; DB 1; Length 398;
Best Local Similarity 83.3%; Pred. No. 3e-137;
Matches 335; Conservative 21; Mismatches 40; Indels 6; Gaps 4;
QY 1 MAVLSAADASPVSAGIFEGYKLEITFSEAPVFDVDPHGRLRALSGRAQIDSVLDLART 60
DB 1 MGVLSAADPPVSAIGFEGYKLEITFSEAPVFDVDPHGRLRALSGRAQIDSVLDLART 60
QY 61 IVSELSNKFDSYLVSESSIFLYPLKIVIKTCCTTKLLLTIPRIELAEELSPLAAVKY 120
DB 61 IVSELSNKFDSYLVSESSIFLYPLKIVIKTCCTTKLLLTIPRIELAEELSPLAAVKY 120
QY 121 SRTGTFPGAQAPAPHSFSEVAALNRYFGGLKSGGNVYIGDPPARPGQKWHVYFATEYP 180
DB 121 SRTGTFPGAQAPAPHSFSEVAALNRYFGGLKSGGNVYIGDPPARPGQKWHVYFATEYP 180
QY 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
DB 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
QY 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSEFSVAV 300
DB 241 GYSMNAIHGSAFSTIHTVTPEDGFSYASYEVMGLDATALSYGDLVKRVLRCFGSEFSVAV 300
QY 301 TIFGGRGHAGTWKALGAEVYDNNVVEQLPQGLLVYQSFCAAEADVATSPKSVFHC 358
DB 301 TIFGGRGHAGTWKALGAEVYDNNVVEQLPQGLLVYQSFCAAEADVATSPKSVFHC 358
QY 359 CFGENVESAPPPMKDYKLANLLCWEEBDAAMEEKAGVLDE 400
DB 361 CFEAENMVN-PAPVKEG-KLGNLLPWGE--DALEENDGVFDE 398

RESULT 3
Q7XT83 PRELIMINARY; PRT; 398 AA.
ID Q7XT83; Q7XUL0;
AC Q7XT83; Q7XUL0;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE OSJNBa0029H02.2 protein (OSJNBa0067K08.23 protein).
GN Name=OSJNBa0029H02.2; Synonyms=OSJNBa0067K08.23;
OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12447439; DOI=10.1038/nature01183;
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Wang R., Jin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.,
 RT "Sequence and analysis of rice chromosome 4."
 RL Nature 420:316-320(2002).
 DR EMBL; AL606594; CAB01625.2; -;
 DR HSP; AL606627; CAB01624.2; -;
 DR HSP; P17707; 117B.
 DR Gramene; Q7XT83; -;
 DR Gramene; Q7XU0; -;
 DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
 DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
 DR GO; GO:0006597; P:spermine biosynthesis; IEA.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 SQ SEQUENCE 398 AA; 43283 MW; BC24F359962F8655 CRC64;

Query Match 81.8%; Score 1715; DB 2; Length 398;
 Best Local Similarity 83.3%; Pred. No. 3e-137;
 Matches 335; Conservative 21; Mismatches 40; Indels 6; Gaps 4;

QY 1 MAVLSAADAPVSAIGPEGYKLEITFSAPVDPHGRLRALRAQIDSVLDLART 60
 DB 1 MGVLAAADPPVSAIGPEGYKLEITFSAPVDPHGRLRALRAQIDSVLDLART 60
 QY 61 IVSELSNKPDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 120
 DB 61 IVSELSNKPDSYVLSSESLFIYDKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY 120
 QY 121 SRGTFTPPGAQAPHRFSFEVVAALNRYFGLKSGGNAYVIGDPAPGQKWHFYATEYP 180
 DB 121 SRGFTFPFSAQAPHRFSFEVVAALNRYFGLKSGGNAYVIGDPAPGQKWHFYATQHP 180
 QY 181 EQPMVNLWCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
 DB 181 EQPMVNLWCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPC 240
 QY 241 GYSNNAIHGSAFSTIHTVTPDGFSGYSAYEVWGLDATALSYGDLVLRVLCFGPSEFSVAV 300
 DB 241 GYSNNAIHGSAFSTIHTVTPDGFSGYSAYEVWGLDATALSYGDLVLRVLCFGPSEFSVAV 300
 QY 301 TIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGLLLVYQSCAAED--AVATSPKSVFH 358
 DB 301 TIFGGRHAGTWGKALGAEVYDCNNMVQEQLPGGLLLVYQSCAAED--AVATSPKSVFH 358
 QY 359 CFQGENVESAPPKMDYKLANLLCWEEADAMEEKAGVLDE 400
 DB 361 CFQENMVN--PAPVKEG-KLGNLLPWGE--DALEENDGVFDE 398

RESULT 4
 DCAM_HORCH
 ID _DCAM_HORCH
 AC Q42829;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
 DE (Samdc) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-
 DE adenosylmethionine decarboxylase beta chain].
 GN Name=SAMDC;
 OS Hordeum chilense (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=15565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=96270379; PubMed=86399739;
 RA Dresselhaus T., Barcelo P., Hagel C., Loerz H., Humbeck K.,
 RT "Isolation and characterization of a Tritordeum cDNA encoding S-
 RT adenosylmethionine decarboxylase that is circadian-clock-regulated.";
 RL Plant Mol. Biol. 30:1021-1033(1996).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-
 CC adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
 CC -1- COFACTOR: Pyruvoyl group.
 CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
 CC aminopropyl moiety required for spermidine and spermine
 CC biosynthesis from putrescine.
 CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
 CC -----
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DR EMBL; X83881; CAAS8762.1; -;
 DR PIR; S69191; S69191.
 DR HSP; P17707; 1JEN.
 DR InterPro; IPR001985; SAM decarbox.
 DR Pfam; PF01536; SAM decarbox; 1.
 DR ProDom; PD002379; SAM decarbox; 1.
 DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
 DR PROSITE; PS01336; ADOMETDC; 1.
 KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
 FT FT S-adenosylmethionine decarboxylase beta
 FT CHAIN 1 70 chain (By similarity).
 FT FT S-adenosylmethionine decarboxylase alpha
 FT CHAIN 71 393 chain (By similarity).
 FT SITE 70 71 Cleavage (nonhydrolytic) (By similarity).
 FT MOD_RES 71 71 Pyruvic acid (Ser) (By similarity).
 FT ACT_SITE 11 11 By similarity.
 FT ACT_SITE 14 14 By similarity.
 FT ACT_SITE 85 85 By similarity.
 SQ SEQUENCE 393 AA; 42895 MW; 6CD1AA94792AF6CB CRC64;

Query Match 80.2%; Score 1682.5; DB 1; Length 393;
 Best Local Similarity 82.7%; Pred. No. 1.7e-134;
 Matches 324; Conservative 25; Mismatches 38; Indels 5; Gaps 3;

QY 9 ASPVSAIGEGYKRLIETFSAPVDPHGRLRALRAQIDSVLDLARTIVSELSNK 68
 DB 2 AAPVSAIGEGYKRLIETFSAPVDPHGRLRALRAQIDSVLDLARTIVSELSNK 61
 QY 69 DFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRILELAELSPLAAVKYSGRTGTFP 128
 DB 62 DFDSYVLSSESLFIYQKIVIKTCGTTKLLLTIPRILELAELSPLAAVKYSGRTGTFP 121
 QY 129 GAQAPHRFSFEVVAALNRYFGLKSGGNAYVIGDPAPGQKWHFYATEYPQPMVNL 188
 DB 122 GAQAPHRFSFEVVAALNRYFGLKSGGNAYVIGDPAPGQKWHFYATEYPQPMVNL 181
 QY 189 MCMTGDKKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPCGYSMNAIH 248
 DB 182 MCMTGDKKKACVFFKTNADGNTTCAKEMTKLSGISEIIPEMEICDFDFEPCGYSMNAIH 241

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Qy 249 GSAFSTHVTPEGFSYASVEVMGLDATALSYGDLVKRVLRCRGPSEFSFVAVTIFGGRGH 308
Db 242 GSAFSTHVTPEGFSYASVEVMGLDATALSYGDLVKRVLRCRGPSEFSFVAVTIFGGRGH 301
Qy 309 AGTWGKALGAEDVDCNNVVEQELPGGGLLVYQSFCAEDAV--ATSPKSVFHCDFDGENVE 366
Db 302 AATWGGKLDAAEDVDCNNVVEQELPGGGLLVYQSFCAEDAV--ATSPKSVFHCDFDGENVE 359
Qy 367 SAPPPMKKDYKLANLLCWEEBEEADAMEEKA 398
Db 360 SG-HPLVKEGKLANLLAWRAEEDSLEBGTAL 390

RESULT 5
Q92PJ1 ID Q92PJ1 PRELIMINARY; PRT; 392 AA.
AC Q92PJ1
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DE S-adenosylmethionine decarboxylase.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Z.Y., Chen S.Y.;
RT "Isolation and characterization of a salt and drought-inducible gene
RT for S-adenosylmethionine decarboxylase from wheat (Triticum aestivum
RL L.).";
RL J. Plant Physiol. 156:386-393 (2000).
DR EMBL; AF117660; AAD17232.1; -.
DR HSP; P17707; IJEN
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 392 AA; 42854 MW; C761765631C2B91F CRC64;

Query Match 79.3%; Score 1663; DB 2; Length 392;
Best Local Similarity 81.7%; Pred. No. 7.8e-133;
Matches 318; Conservative 26; Mismatches 41; Indels 4; Gaps 2;

Qy 9 ASPVSAIGFEGYEKRLKLTITSEAPVFDPHGRGLRALSRQAIDSVDLRLACTIVSELSTK 61
Db 2 AAPTSAIGFEGYEKRLKLTITSEAPVFDPHGRGLRALSRQAIDSVDLRLACTIVSELSTK 61
Qy 69 DFDYVLSSESLFIYPLKIVIKTCGTTKLLTIPRILELAELSMPAAVKYRGFIFF 128
Db 62 DFDYVLSSESLFIYQKIVIKTCGTTKLLTIPRILELAELSMPAAVKYRGFIFF 121
Qy 129 GAOPAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEPQPMWNLE 188
Db 122 GAOPAPHRSPSEVVDVNLNRYFGHLKSGGNAYVIGDPAKQKWHVYATYEPQPMWNLE 181
Qy 189 MCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDPDFPCGYSMAIH 248
Db 182 MCMTGLDKKASVFFKTDASHVSCAKEMTKLSGISDIIPEMEICDPDFPCGYSMAIN 241
Qy 249 GSAFSTHVTPEGFSYASVEVMGLDATALSYGDLVKRVLRCRGPSEFSFVAVTIFGGRGH 308
Db 242 GSAFSTHVTPEGFSYASVEVMGLDATALSYGDLVKRVLRCRGPSEFSFVAVTIFGGRGH 301
Qy 309 AGTWGKALGAEDVDCNNVVEQELPGGGLLVYQSFCAEDAV--ATSPKSVFHCDFDGENVE 366
Db 302 AATWGGKLDAAEDVDCNNVVEQELPGGGLLVYQSFCAEDAV--ATSPKSVFHCDFDGENVE 361

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Qy 367 SAPPPMKKDYKLANLLCWEEBEEADAMEEKA 395
Db 362 S-HPLVKEGKLANLLAWRAEEDSLEBGA 388

RESULT 6
Q6K9B8 ID Q6K9B8 PRELIMINARY; PRT; 395 AA.
AC Q6K9B8
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE S-adenosylmethionine decarboxylase 2.
OS Name=OJ1476 F05.33; Synonyms=OJ1004 A05.7;
OS Oryza sativa (japonica cultivar-group)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004063; BAD19232.1; -.
DR EMBL; AP005286; BAD19677.1; -.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 395 AA; 43152 MW; 49C9BC56F20FE540 CRC64;

Query Match 77.8%; Score 1632; DB 2; Length 395;
Best Local Similarity 79.3%; Pred. No. 3.4e-130;
Matches 314; Conservative 26; Mismatches 46; Indels 10; Gaps 2;

Qy 1 MAVLSAADASPVSAIGFEGYEKRLKLTITSEAPVFDPHGRGLRALSRQAIDSVDLRLACT 60
Db 1 MAVLSVADSPVSAIGFEGYEKRLKLTITSEAPVFDPHGRGLRALSRQAIDSVDLRLACT 60
Qy 61 IVSELSNKDPSVLSSESLFIYPLKIVIKTCGTTKLLTIPRILELAELSMPAAVKY 120
Db 61 IVSELSNEVFDVLSSESLFIYVYKIVIKTCGTTKLLTIPRILELAELSMPAAVKY 120
Qy 121 SRTGTFIPGAPAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP 180
Db 121 SRTGTFIPGAPAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPAKQKWHVYATYEP 180
Qy 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDPDFPC 240
Db 181 EQPMVNLKMTGLDKKASVFFKTDASHVSCAKEMTKLSGISDIIPEMEICDPDFPC 240
Qy 241 GYSMNAIHGSAFSTHVTPEGFSYASVEVMGLDATALSYGDLVKRVLRCRGPSEFSVAV 300
Db 241 GYSMNAIHGSAFSTHVTPEGFSYASVEVMGLDATALSYGDLVKRVLRCRGPSEFSVAV 300
Qy 301 TIFGGRGHAGTWGKALGAEDVDCNNVVEQELPGGGLLVYQSFCAEDAVATSPKSVFHC 360
Db 301 TIFGGRGHAGTWGKALGAEDVDCNNVVEQELPGGGLLVYQSFCAEDAVATSPKSVFHC 360
Qy 361 DGENVTSAPPPMKKDYKLANLLCWEEBEEADAMEEKA 396
Db 361 ADENKTEKAGK-----MEALYWD-----DAVEIDG 386

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RESULT 7	Q9SC67	PRELIMINARY;	PRT;	395 AA.
ID	Q9SC67	Q9SC67		
AC	Q9SC67	Q9SC67		
DT	01-MAY-2000	(T-EMBLrel. 13, Created)		
DT	01-MAY-2000	(T-EMBLrel. 13, Last sequence update)		
DT	01-JUN-2003	(T-EMBLrel. 24, Last annotation update)		
DE	S-adenosylmethionine decarboxylase 2 (BC 4.1.1.50).			
GN	Names=admetDC2;			
OS	Oryza sativa (rice).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzaceae; Oryza.			
OX	NCBI_TaxID=4530;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21066059; PubMed=11139406; DOI=10.1042/0264-6021:3530403;			
RA	Franceschetti M., Hanfrey C., Scaramagli S., Torrigiani P., Bagni N.,			
RA	Michael A.J.;			
RT	"Characterization of monocot and dicot plant S-adenosyl--methionine			
RT	decarboxylase gene families including identification in the mRNA of a			
RT	highly conserved pair of upstream overlapping open reading frames.";			
RL	Biochem J. 353:403-409(2001).			
DR	EMBL; AJ251899; CAB64600.1; -.			
DR	HSSP; P17707; 1JEN.			
DR	Gramene; Q9SC67; -.			
DR	GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.			
DR	GO; GO:0016829; F:lyase activity; IEA.			
DR	GO; GO:0008295; P:spermidine biosynthesis; IEA.			
DR	GO; GO:0006597; P:spermine biosynthesis; IEA.			
DR	InterPro; IPR001985; SAM decarbox.			
DR	Pfam; PF01536; SAM decarbox; 1.			
DR	ProDom; PD002379; SAM decarbox; 1.			
DR	TIGRFAMs; TIGR00535; SAM DCcase; 1.			
DR	PROSITE; PS01336; ADOMETDC; 1.			
KW	lyase.			
SQ	SEQUENCE 395 AA; 43152 MW; 49C9BC56F20F540 CRC64;			
Query Match 77.8%; Score 1632; DB 2; Length 395;				
Best Local Similarity 79.3%; Pred. No. 3.4e-130;				
Matches 314; Conservative 26; Mismatches 46; Indels 10; Gaps 2;				
QY	1	MAVLSAADSPVSAIGFEGYKRLTFTSEAPVFDPHGRGLRALSRQAQIDSVLDLARCT	60	
DB	1	MAVLSVADSPVSAIGFEGYKRLTFTSEAPVFDPHGRGLRALSRQAQIDSVLDLARCT	60	
QY	61	IVSELSNKKDFDSVYLSSESLFYPLKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY	120	
DB	61	IVSELSNEVFDVYLSSESLFYPLKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY	120	
QY	121	SRGTFIFPGAQAPHRSPFSEVAALNRYFGGLKSGGNAYVIGDPAPGKQWHVYATEYP	180	
DB	121	SRGTFIFPGAQAPHRSPFSEVAALNRYFGGLKSGGNAYVIGDPAPGKQWHVYATEYP	180	
QY	181	EQPMVNLKMTGLDKKKACVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC	240	
DB	181	EQPVVTLKMTGLDKKKASVFFKTDGHTTAKEMTKLSGISEIIPEMEICDFDFEPC	240	
QY	241	GYSMNAIHGSAFTIHTVTPEDGFSYASYEVWGLDATALSYGDLVKRVLRCFGSPFSVAV	300	
DB	241	GYSMNAIHGSAFTIHTVTPEDGFSYASYEVWGLDATALSYGDLVKRVLRCFGSPFSVAV	300	
QY	301	TIFGGRHAGTWKALCAEYVDYCNMNVQELPQGLLVVQSCAAEDAVATSPKSPHCF	360	
DB	301	TIFGGRHAGTWKALCAEYVDYCNMNVQELPQGLLVVQSCAAEDAVATSPKSPHCF	360	
QY	361	DGENVESAPPPMKDYKLANLLCWEEBEEADAMEEKA 396		
DB	361	ADENTEKAGK-----MEALYED--DAVERIDG 386		
RESULT 8	Q6F4N6	PRELIMINARY;	PRT;	392 AA.
ID	Q6F4N6	Q6F4N6		
AC	Q6F4N6	Q6F4N6		
DT	25-OCT-2004	(T-EMBLrel. 28, Created)		
DT	25-OCT-2004	(T-EMBLrel. 28, Last sequence update)		
DT	25-OCT-2004	(T-EMBLrel. 28, Last annotation update)		
DE	S-adenosylmethionine decarboxylase.			
GN	Names=SAMDC1; Synonyms=P0418B08.27-1;			
OS	Oryza sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzaceae; Oryza.			
OX	NCBI_TaxID=39947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15215597;			
RA	Yamaguchi T., Nakayama K., Hayashi T., Yazaki J., Kishimoto N.,			
RA	Kikuchi S., Koike S.;			
RT	"cDNA Microarray Analysis of Rice Anther Genes under Chilling Stress			
RT	at the Microsporogenesis Stage Revealed Two Genes with DNA Transposon			
RT	Castaway in the 5'-Flanking Region.";			
RL	Biosci. Biotechnol. Biochem. 68:1315-1323(2004).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Sasaki T., Matsumoto T., Katayose Y.;			
RT	"Oryza sativa nipponbare (GAJ) genomic DNA, chromosome 9, PAC			
RT	clone: P0418B08.";			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB122089; BAD26704.1; -.			
DR	EMBL; AP005420; BAD33432.1; -.			
DR	GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.			
DR	GO; GO:0008295; P:spermidine biosynthesis; IEA.			
DR	GO; GO:0006597; P:spermine biosynthesis; IEA.			
DR	InterPro; IPR001985; SAM decarbox.			
DR	Pfam; PF01536; SAM decarbox; 1.			
DR	ProDom; PD002379; SAM decarbox; 1.			
DR	TIGRFAMs; TIGR00535; SAM DCcase; 1.			
DR	PROSITE; PS01336; ADOMETDC; 1.			
SQ	SEQUENCE 392 AA; 42717 MW; 0DF1F61522C38FE3 CRC64;			
Query Match 64.7%; Score 1357; DB 2; Length 392;				
Best Local Similarity 67.6%; Pred. No. 8.4e-107;				
Matches 267; Conservative 47; Mismatches 71; Indels 10; Gaps 5;				
QY	4	LSAAD---ASPVSAIGFEGYKRLTFTSEAPVFDPHGRGLRALSRQAQIDSVLDLARCT	60	
DB	3	MSLADSWGSPASPIGFEYKRLTFTSDAPVFDPCGRLRALSRQAQIDSVLDLARCT	62	
QY	61	IVSELSNKKDFDSVYLSSESLFYPLKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY	120	
DB	63	IVSHLSNKHFDVYLSSESLFYPLKIVIKTCGTTKLLLTIPRILELAELSPLAAVKY	122	
QY	121	SRGTFIFPGAQAPHRSPFSEVAALNRYFGGLKSGGNAYVIGDPAPGKQWHVYATEYP	180	
DB	123	SRGMFIFPGAQSPHRSPFSEVSLNRYFGGLKSGGNAYVIGDAFPKQKWHVYATEYP	182	
QY	181	EQPMVNLKMTGLDKKKACVFFKTNADGNNTTCAKEMTKLSGISEIIPEMEICDFDFEPC	240	
DB	183	EQPVVTLKMTGLDKKAAEVFFKTDGSCSSAKEMTWFGISEIIPEMEICDFDFEPC	242	
QY	241	GYSMNAIHGSAFTIHTVTPEDGFSYASYEVWGLDATALSYGDLVKRVLRCFGSPFSVAV	300	
DB	243	GYSMNGIYGPVAVSTIHTVTPEDGFSYASYEVWGLDATALSYGDLVKRVLRCFGSPFSVAV	302	
QY	301	TIFGGRHAGTWKALCAEYVDYCNMNVQELPQGLLVVQSCAAEDAVATSPKSPHCF	360	
DB	303	TIFGGRHAGTWKALCAEYVDYCNMNVQELPQGLLVVQSCAAEDAVATSPKSPHCF	360	
QY	361	DGENVESAPPPMKDYKLANLLCWEEBEEADAMEEKA 395		
DB	359	DGWNSDGA-EMVAKSKEMS--VCWEGEKAAXKDA 390		
RESULT 9				

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Q84LA2
ID Q84LA2 PRELIMINARY; PRT; 370 AA.
AC Q84LA2;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE S-adenosylmethionine decarboxylase.
GN Name=SAMdc;
OS Narcissus pseudonarcissus (Daffodil).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=4-day old flower tepals;
RA Gookin T.E., Cabauatan E.V., Hunter D.A., Reid M.S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232672; AA043186.1; -.
DR HSSP; P17707; IJEN
SQ SEQUENCE 370 AA; 40680 MW; 36F619BA4806F70F CRC64;
Query Match 63.8%; Score 138.5; DB 2; Length 370;
Best Local Similarity 69.1%; Pred. No. 2.9e-105;
Matches 250; Conservative 47; Mismatches 64; Indels 1; Gaps 1;
Qy 13 SAIGFEGYKRLRITFEAPVFDVDPHGRGLRALSRQIDSILDLARCTIVDSLNKDFDS 72
Db 7 SPIGFEGYKRLRITFEAPVFDVDPHGRGLRALSRQIDSILDLARCTIVDSLNKDFDS 66
Qy 73 YVLSSESLFYPIKVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 132
Db 67 YVLSSESLFYPIKVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 126
Qy 133 AHRSESEVAALNRVFGGLKSGNAVIGDPPRGKLVHVFYATEYPEOPMNLKMT 192
Db 127 TPRNSEEVSALDHFGNLAGSGNAVIGDPPSPRNWHIYATQKPELPTVLEKMT 186
Qy 193 GLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAF 252
Db 187 GLDSEKASIFFNSPGNANNAQSKMTKLSGISNIIPEMEICDFDFPCGYSMNAICGSAH 246
Qy 253 STIHVTPEDGFSYASVEVMGLDATALSYGLVKRVLRCFSPSEFSAVATIFGGRGHAGTW 312
Db 247 STIHVTPEDGSSYASVEAMGFNPAELDFGLVVERVLECFGDFSAVATIFGGRGQAGSW 306
Qy 313 GKALGAEVYDCNNMVQELPGGGLLVYQSCAAEDAVATSPKSVHCFDGENVESAPPPM 372
Db 307 GREVDSYGRFCDVLEQELAGGLLMYQSTAGVRMG-SPRSTLHCWDGEEIEEKKAED 365
Qy 373 KK 374
Db 366 KK 367
RESULT 10
Q944U3
ID Q944U3 PRELIMINARY; PRT; 369 AA.
AC Q944U3;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE S-adenosyl-L-methionine decarboxylase.
GN Name=Samdc;
OS Dendrobium crumenatum (Tropical pigeon orchid).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Narcissus.
OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=4-day old flower tepals;
RA Gookin T.E., Cabauatan E.V., Hunter D.A., Reid M.S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232672; AA043186.1; -.
DR HSSP; P17707; IJEN
SQ SEQUENCE 370 AA; 40680 MW; 36F619BA4806F70F CRC64;
Query Match 63.8%; Score 138.5; DB 2; Length 370;
Best Local Similarity 69.1%; Pred. No. 2.9e-105;
Matches 250; Conservative 47; Mismatches 64; Indels 1; Gaps 1;
Qy 13 SAIGFEGYKRLRITFEAPVFDVDPHGRGLRALSRQIDSILDLARCTIVDSLNKDFDS 72
Db 7 SPIGFEGYKRLRITFEAPVFDVDPHGRGLRALSRQIDSILDLARCTIVDSLNKDFDS 66
Qy 73 YVLSSESLFYPIKVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 132
Db 67 YVLSSESLFYPIKVIKTCGTTKLLTIPRIELEAEELSMPLAAVKYSGRTIFPGAQP 126
Qy 133 AHRSESEVAALNRVFGGLKSGNAVIGDPPRGKLVHVFYATEYPEOPMNLKMT 192
Db 127 TPRNSEEVSALDHFGNLAGSGNAVIGDPPSPRNWHIYATQKPELPTVLEKMT 186
Qy 193 GLDKKACVFFKTNADGNTTCAKEMTKLSGISIIPEMEICDFDFPCGYSMNAIHGSAF 252
Db 187 GLDSEKASIFFNSPGNANNAQSKMTKLSGISNIIPEMEICDFDFPCGYSMNAICGSAH 246
Qy 253 STIHVTPEDGFSYASVEVMGLDATALSYGLVKRVLRCFSPSEFSAVATIFGGRGHAGTW 312
Db 247 STIHVTPEDGSSYASVEAMGFNPAELDFGLVVERVLECFGDFSAVATIFGGRGQAGSW 306
Qy 313 GKALGAEVYDCNNMVQELPGGGLLVYQSCAAEDAVATSPKSVHCFDGENVESAPPPM 372
Db 307 GREVDSYGRFCDVLEQELAGGLLMYQSTAGVRMG-SPRSTLHCWDGEEIEEKKAED 365
Qy 373 KK 374
Db 366 KK 367
RESULT 11
Q9FSM2
ID Q9FSM2 PRELIMINARY; PRT; 319 AA.
AC Q9FSM2;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE S-adenosylmethionine decarboxylase.
GN Name=H0711G06.28;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Mu J., Zhou B., Chen Z.H., Li Y., Zhu J.J.,
RA Tang Y.S., Zhao Q., Liu Y.L., Huang Y.C., Yu Z., Fan D.L., Chen L.,
RA Wang Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X.,

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RA Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
RA Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL442115; CAC09522.1; -
DR HSSP; P17707; I178.
DR Gramene; Q9FSM2; -.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
SQ SEQUENCE 319 AA; 34854 MW; B0648B852F74A8E1 CRC64;

Query Match 61.5%; Score 1290; DB 2; Length 319;
Best Local Similarity 89.6%; Pred. No. 3.2e-101;
Matches 249; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 MAVLSAADASPVSIAIGFEGYEKRLITFSEAPVFDPHGRLRALRAQIDSVLDLART 60
DB 37 MGVLSSAADPPVSAIGFEGYEKRLITFSEAPVFDPHGRLRALRAQIDSVLDLART 96
QY 61 IVSELNKPDSVYLSSESLFIYPLKIVIKTCGTTKLLTIPRIELABELSMPLAAVKY 120
DB 97 IVSELNKPDSVYLSSESLFIYSDKIVIKTCGTTKLLTIPRIELABELSMPLAAVKY 156
QY 121 SRGTFFPGQAAPHRSFSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKWHVFYATEYP 180
DB 157 SRGTFPPSAQAAPHRSFSEVAALNRYFGHLKSGGNAYVIGDPAAPGQKWHYIYATQHP 216
QY 181 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFEPC 240
DB 217 EQPMVNLKMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFEPC 276
QY 241 GYSMAIHGSAFSTIHVTPEDGFSYASVEYVMDLATAL 278
DB 277 GYSMAIHGSAFSTIHVTPEDGFSYASVEYVMDLALL 314

RESULT 12
QY 07XZ09 PRELIMINARY; PRT; 358 AA.
AC 07XZ09;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50).
GN Names=andc;
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Vitaceae; Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Tassoni A., Accattulli P., Bagni N.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ567368; CAD98785.1; -.
DR HSSP; P17707; IJEN.
DR GO; GO:0004014; F:adenosylmethionine decarboxylase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008295; P:spermidine biosynthesis; IEA.
DR GO; GO:0006597; P:spermine biosynthesis; IEA.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM_DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Lyase.
FT CHAIN 2 358 S-adenosylmethionine decarboxylase.

SQ SEQUENCE 358 AA; 39783 MW; E6037EDA79132AE3 CRC64;

Query Match 47.7%; Score 1000; DB 2; Length 358;
Best Local Similarity 53.4%; Pred. No. 1.8e-76;
Matches 211; Conservative 51; Mismatches 85; Indels 48; Gaps 9;

QY 9 ASFVSAIGFEGYEKRLITFSEAPVFDPHGRLRALRAQIDSVLDLARTTIVSLSNK 68
DB 2 ALPVSIAIGFEGYEKRLITFSEAPVFDPHGRLRALRAQIDSVLDLARTTIVSLSND 61
QY 69 DFDSVYLSSESLFIYPLKIVIKTCGTTKLLTIPRIELABELSMPLAAVKYSGTFIPP 128
DB 62 IVDSVYLSSESLFIYVYPIKIIKTCGTTKLLTIPRIELABELSMPLAAVKYSGTFNFP 121
QY 129 GAQPAHRFSFSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKWHVF-YATEYP--BQPMV 185
DB 122 GAQPYPHRFSEVAALNRYFGGLKSGGNAYVIGDPAAPGQKWHVFYATEYP--BQPMV 180
QY 186 NLEMCWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFEPCGYSMN 245
DB 181 TLEMCWTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFEPCGYSMN 236
QY 246 AHHGSAFSTIHVTPEDGFSYASVEYVMDLATALSYGDLVKRLVLCFSPSEFSAVATIFGG 305
DB 237 AHHGSAFSTIHVTPEDGFSYASVEYVMDLATALSYGDLVKRLVLCFSPSEFSAVATIFGG 291
QY 306 RGHAGTWGK-----ALGAEVYDCNNMVEQLPGGGLLVYQSFCAAEADAVATSPKSVFHC 359
DB 292 --HADISGKLLERNCLLDVKGCCERSNEELCMCGSMVYHRPMTKTEGLV--SPRSILKC 347
QY 360 PDGENVESAPPMKKDYKLANLLCWEEEDADAMEEK 394
DB 348 -----CWKEEEE--EEK 357

RESULT 13
DCAM CATRO STANDARD; PRT; 357 AA.
AC 042679;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
GN Name=SamDC;
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
OC Catharanthus.
OX NCBI_TaxID=4059;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-71.
RA MEDLINE=95188916; PubMed=7883014;
RX Schroeder G., Schroeder J.;
RT "cDNA for S-adenosyl-L-methionine decarboxylase from Catharanthus roseus, heterologous expression, identification of the proenzyme-processing site, evidence for the presence of both subunits in the active enzyme, and a conserved region in the 5' mRNA leader.";
RL Eur. J. Biochem. 228:74-78(1995).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S)-deoxy-5-adenosyl (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -1- COFACTOR: Pyruvoyl group.
CC -1- PATHWAY: decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
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DR EMBL; U12573; AAC48989.1; -.
DR PIR; S68990; S68990.
DR HSSP; P17707; 1JEN.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 70 S-adenosylmethionine decarboxylase beta
FT chain.
FT CHAIN 71 357 S-adenosylmethionine decarboxylase alpha
FT chain.
FT SITE 70 71 Cleavage (nonhydrolytic).
FT MOD_RES 71 71 Pyruvic acid (Ser).
FT ACT_SITE 11 11 By similarity.
FT ACT_SITE 14 14 By similarity.
FT ACT_SITE 85 85 By similarity.
FT MUTAGEN 71 S->A: Loss of activity.
SQ SEQUENCE 357 AA; 39714 MW; 364918E116388301 CRC64;

Query Match 46.7%; Score 980; DB 1; Length 357;
Best Local Similarity 51.6%; Pred. No. 8.8e-75;
Matches 204; Conservative 56; Mismatches 87; Indels 48; Gaps 8;

QY 9 ASPVSAIGFEGYKRLLEITFSEAPVFDPHGRGLRALSRAQIDSVLDLARCTIVSELSNK 68
DB 2 ALPASAIGFEGYKRLLEISFFESFPADPDGKGLRALNKSQIDLEILPAECTIVDSLSNQ 61

QY 69 DFDYVLSSESLFIYPLKIVIKTCGTTKLLLTTPRILELAELSMLPAAVKYSGRTFIPP 128
DB 62 YLDSYVLSSESLFIYPKIITKTCGTTKLLSIPAILKLAESLSVRNVKYYTRGSPFIP 121

QY 129 GAQPAPHRSEVAALNRYFGLKSGNAYVGDPAKQKWHVYATPEQ---PMV 195
DB 122 GAQSPFHRSEVAALNRYFGLKSGNAYVGDPAKQKWHVYATPEQ---PMV 180

QY 186 NLEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFPCGYSMN 245
DB 181 TLEMCMTGLDREKASVYFKS----ESSAALMTTRSGIRKILPDSICDFEPCGYSMN 236

QY 246 AIHGSFSTHTVTPEDGFSYASVEVMDLATALSYGDLVKRVLRCFGPSEFSVAVTFGG 305
DB 237 SIEEAAISTHTVTPEDGFSYASFEAAGYDLKAQNLGMIVRLVACQPSEFSVAV---- 291

QY 306 RGHAGTWGK-----ALGAEVYDNNMVEQLPGGGLLVYQSFCAAEADAVATSPKSVFHC 359
DB 292 --HCDVTCKSLQICSLKEYSLDEKINELGLGGSIYKFLRID--ACGSPRSLKC 347

QY 360 FDGENVESAPPMKKDYKLANLLCWEEADAMEEK 394
DB 348 -----CWKE--DESEEE 357

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RESULT 14
DCAM_NICSY
ID DCAM_NICSY STANDARD; PRT; 361 AA.
AC 080402;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
DE Name=SAMDC1; Synonyms=SAMDC-1;
GN Nicotiana sylvestris (wood tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.

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OX NCBI_TaxID=4096;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakakita M.;
RT "Putative cDNA for S-adenosylmethionine decarboxylase from Nicotiana
sylvestris.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl)-methylsulfonium salt + CO(2).
CC -|- COFACTOR: Pyruvoyl group (By similarity).
CC -|- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
CC -|- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
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DR EMBL; AB015609; BAA29040.1; -.
DR HSSP; P17707; 1JEN.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRFAMs; TIGR00535; SAM DCase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
FT CHAIN 1 72 S-adenosylmethionine decarboxylase beta
FT chain (By similarity)
FT CHAIN 73 361 S-adenosylmethionine decarboxylase alpha
FT SITE 72 73 Cleavage (nonhydrolytic) (By similarity).
FT MOD_RES 73 73 Pyruvic acid (Ser) (By similarity).
FT ACT_SITE 13 13 By similarity.
FT ACT_SITE 16 16 By similarity.
FT ACT_SITE 87 87 By similarity.
FT ACT_SITE 87 87 By similarity.
SQ SEQUENCE 361 AA; 39681 MW; 648EB2F6CC61FFE CRC64;

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Query Match 46.2%; Score 969; DB 1; Length 361;
Best Local Similarity 51.4%; Pred. No. 7.7e-74;
Matches 203; Conservative 49; Mismatches 97; Indels 46; Gaps 7;

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QY 9 ASPVSAIGFEGYKRLLEITFSEAPVFDPHGRGLRALSRAQIDSVLDLARCTIVSELSNK 68
DB 4 ALPASAIGFEGYKRLLEISFFESFPADPDGKGLRALSRAQIDSVLDLARCTIVDSLSND 63

QY 69 DFDYVLSSESLFIYPLKIVIKTCGTTKLLLTTPRILELAELSMLPAAVKYSGRTFIPP 128
DB 64 DFDYVLSSESLFIYPKIITKTCGTTKLLSIPAILKLAETLSLVRNVKYYTRGSPFIP 123

QY 129 GAQPAPHRSEVAALNRYFGLKSGNAYVGDPAKQKWHVYATPEQ---PMV 185
DB 124 GAQSPFHRSEVAALNRYFGLKSGNAYVGDPAKQKWHVYATPEQ---PMV 182

QY 186 NLEMCMTGLDKKACVFFKTNADGNTTCAKEMTKLSGISEIIPMEICDPDFPCGYSMN 245
DB 183 TLEMCMTGLDREKASVYFKTEG-----SSAAHMTVRSGIRKILPNSBEICDFEPCGYSMN 238

QY 246 AIHGSFSTHTVTPEDGFSYASVEVMDLATALSYGDLVKRVLRCFGPSEFSVAVTFGG 305
DB 239 STEGAALSTHTVTPEDGFSYASFEAAGYDKMTKMLGVLVRLVACPEPDEFSFAL----- 293

QY 306 RGHAGTWGKAL-----GAEVYDNNMVEQLPGGGLLVYQSFCAAEADAVATSPKSVFHC 359
DB 294 --HADVATKLLERVCSDVKGYSLAEWSPEEFKGGSIYVQKF--TRTPFCGSPKSVLKG 349

QY 360 FDGENVESAPPMKKDYKLANLLCWEEADAMEEK 394
DB 350 -----CWKEDEEKEE 361

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RESULT 15
DCAM_TOBAC
ID_DCM TOBAC STANDARD; PRT; 361 AA.
AC O04009; O49005;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (samDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
GN Name=samDC;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Xanthi;
RA Paramale S.R.; Ernst S.G.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=cv. Xanthi;
RA Paramale S.R.; Ernst S.G.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-adenosyl)(3-aminopropyl)-methylsulfonium salt + CO(2).
CC -1- COFACTOR: Pyruvoyl group (By similarity).
CC -1- PATHWAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
CC -1- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
CC
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CC
DR EMBL; U91924; AAB51301.1; -
DR EMBL; AF033100; AAB8854.1; -
DR PIR; T01934; T01934.
DR HSSP; P17707; IJEN.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR ProDom; PD002379; SAM decarbox; 1.
DR TIGRPFAMs; TIGR00535; SAM_DCcase; 1.
DR PROSITE; PS01336; ADOMETDC; 1.
KW Decarboxylase; Lyase; Pyruvate; Spermidine biosynthesis; Zymogen.
CHAIN 1 72 S-adenosylmethionine decarboxylase beta chain (By similarity).
CHAIN 73 361 S-adenosylmethionine decarboxylase alpha chain (By similarity).
SITE 72 73 Cleavage (nonhydrolytic) (By similarity).
MOD_RES 73 73 Pyruvic acid (Ser) (By similarity).
ACT_SITE 13 13 By similarity.
ACT_SITE 16 16 By similarity.
ACT_SITE 87 87 By similarity.
CONFLICT 285 285 E -> Q (in Ref. 2).
CONFLICT 308 308 V -> L (in Ref. 2).
SQ SEQUENCE 361 AA; 39637 MW; 119AE5D256545461 CRC64;
Query Match 46.2%; Score 969; DB 1; Length 361;
Best Local Similarity 51.4%; Pred No. 7.7e-74;
Matches 203; Conservative 49; Mismatches 97; Indels 46; Gaps 7;

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QY

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Db 4 ALPVSALGPEGFEKRLIEISFFEPGLFADPNKGKLSKLAQLDEILGPASCTIVDSLSND 63
QY 69 DFDSYVLSSESLFIYPLKIVIKTCGTTKLLLTIPRIELAEELSMPLAAVKYSRGTFIFP 128
Db 64 DVDSYVLSSESLFIYKIIKTCGTTKLLLTAPPIKLAETLSLKVDVRYRFGSIFFP 123
QY 129 GAQPAPHRSPSEVAALNRYFGGLKSGGNAYVIGDPPARPCQKWHVVFATYVPEQ---PMV 185
Db 124 GAQSFPHRHPSEVAVLVDGYFGKLAAGSKAVIMGSPDK-AQKWHVVSASAGPIQSNDPVY 182
QY 186 NLEMCWTGLDKKACACVFFKTNADGNTTCAKEMTKLSGISEIIPMEMETCDPDPFCGYSMN 245
Db 183 TLEMCWTGLDREKASVFKYKTEG-----SSAAHMTVRSGIRKILNPSEICDFEPEPCGYSMN 238
QY 246 AIGSFAFSTTHVTPEDGFSYASVEVMGLDATALSYGLVXRVLCFCGFSFSFVAVTIFGG 305
Db 239 SIEGAALSTHITPDEGFSYASFEANGYDMTKWKLGLPLVERVLACFPDFEFSSIAL----- 293
QY 306 RGHAGTWGKAL-----GAEVYDCNNMVEQLPGGGLLVYQSFCAAEDAVATSPKSVFHC 359
Db 294 --HADVATKLLERVCSDVKGYSLAEWSPEEFGKGGSIYVKF--TRTPFCGSPKSVLKG 349
QY 360 PDGENVESAPPMKKDYKLANLLCWEEEDAMEEK 394
Db 350 -----CWKEDEEKEEKE 361

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Search completed: May 11, 2005, 22:52:30

Job time : 95.5017 secs

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